

FORM PTO-1390 (Modified) (REV 9-93)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER	
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371				032931-0253	
		U.S. APPLICATION NO. (if known, add 37 C.F.R. 1.53) Unassigned		097/888987	
INTERNATIONAL APPLICATION NO. PCT/CA99/01230		INTERNATIONAL FILING DATE December 23, 1999		PRIORITY DATE CLAIMED December 23, 1998	
TITLE OF INVENTION CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF					
APPLICANT(S) FOR DO/EO/US Andrew D. MURDIN, Raymond P. OOMEN and Joe WANG					
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:					
1.	<input checked="" type="checkbox"/>	This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.			
2.	<input type="checkbox"/>	This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.			
3.	<input type="checkbox"/>	This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).			
4.	<input checked="" type="checkbox"/>	A proper Demand for International Preliminary Examination was made by the 19 <sup>th</sup> month from the earliest claimed priority date.			
5.	<input checked="" type="checkbox"/>	A copy of the International Application as filed (35 U.S.C. 371(c)(2))			
	<input type="checkbox"/>	is transmitted herewith (required only if not transmitted by the International Bureau).			
	<input checked="" type="checkbox"/>	has been transmitted by the International Bureau.			
	<input type="checkbox"/>	is not required, as the application was filed in the United States Receiving Office (RO/US)			
6.	<input type="checkbox"/>	A translation of the International Application into English (35 U.S.C. 371(c)(2)).			
7.	<input checked="" type="checkbox"/>	Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))			
	<input type="checkbox"/>	are transmitted herewith (required only if not transmitted by the International Bureau).			
	<input type="checkbox"/>	have been transmitted by the International Bureau.			
	<input type="checkbox"/>	have not been made; however, the time limit for making such amendments has NOT expired.			
	<input checked="" type="checkbox"/>	have not been made and will not be made.			
8.	<input type="checkbox"/>	A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).			
9.	<input type="checkbox"/>	An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).			
10.	<input type="checkbox"/>	A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).			
11.	<input type="checkbox"/>	Applicant claims small entity status under 37 CFR 1.27.			
Items 12. to 17. below concern other document(s) or information included:					
12.	<input type="checkbox"/>	An Information Disclosure Statement under 37 CFR 1.97 and 1.98.			
13.	<input checked="" type="checkbox"/>	An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.			
14.	<input checked="" type="checkbox"/>	A FIRST preliminary amendment.			
	<input type="checkbox"/>	A SECOND or SUBSEQUENT preliminary amendment.			
15.	<input type="checkbox"/>	A substitute specification.			
16.	<input type="checkbox"/>	A change of power of attorney and/or address letter.			
17.	<input type="checkbox"/>	Other items or information:			

JPL Rec'd PCT/PTO 22 JUN 2001

U.S. APPLICATION NO. <b>097868987</b>		INTERNATIONAL APPLICATION NO. PCT/CA99/01230		ATTORNEY'S DOCKET NUMBER 032931-0253	
18. <input checked="" type="checkbox"/> The following fees are submitted:				<b>CALCULATIONS</b> PTO USE ONLY	
Basic National Fee (37 CFR 1.492(a)(1)-(5): Search Report has been prepared by the EPO or JPO.....\$860.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482).....\$690.00					
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)).....\$710.00					
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO .....\$1,000.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4).....\$100.00					
<b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>				\$860.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than 20 Months from the earliest claimed priority date (37 CFR 1.492(e))					
Claims	Number Filed	Included in Basic Fee	Extra Claims		Rate
Total Claims	39	- 20	= 19	x	\$18.00
Independent Claims	9	- 3	= 6	x	\$80.00
Multiple dependent claim(s) (if applicable)				\$270.00	
<b>TOTAL OF ABOVE CALCULATIONS =</b>				\$1682.00	
Reduction by 1/2 for filing by small entity, if applicable.				\$0.00	
<b>SUBTOTAL =</b>				\$1682.00	
Processing fee of \$130.00 for furnishing English translation later the 20 months from the earliest claimed priority date (37 CFR 1.492(f)).				+	
<b>TOTAL NATIONAL FEE =</b>				\$1682.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +				\$40.00	
<b>TOTAL FEES ENCLOSED =</b>				\$1722.00	
				Amount to be: Refunded \$ Charged \$	
<p>a. <input checked="" type="checkbox"/> A check in the amount of \$1722.00 to cover the above fees is enclosed.</p> <p>b. <input type="checkbox"/> Please charge my Deposit Account No. 19-0741 in the amount of \$.00 to the above fees. A duplicate copy of this sheet is enclosed.</p> <p>c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 19-0741. A duplicate copy of this sheet is enclosed.</p>					
<p>NOTE: (a) where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.</p>					
SEND ALL CORRESPONDENCE TO:					
<p>Foley &amp; Lardner Washington Harbour 3000 K Street, N.W., Suite 500 Washington, D.C. 20007-5109</p>					
<p>SIGNATURE <u><i>[Signature]</i></u></p> <p>NAME MICHELE M. SIMKIN</p> <p>REGISTRATION NUMBER 34,717</p>					

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant: Andrew D. MURDIN, et al.  
Title: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA  
FRAGMENTS AND USES THEREOF  
Application No.: To be assigned (US entry of PCT/CA99/01230)  
Filing Date: December 23, 1999  
Examiner: Unassigned  
Art Unit: Unassigned

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

In accordance with 37 CFR §1.121, please cancel claims 40-78 in their entirety without prejudice or disclaimer and substitute for claims 1-39 in the Annex to the IPER the following rewritten versions of the same claims, as amended. The changes to claims 1-39 are shown explicitly in the attached "marked up claims".

**IN THE CLAIMS:**

1. (Amended) A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any one of:

- (a) SEQ ID Nos: 15 to 26;
- (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

2. (Amended) A nucleic acid molecule comprising a nucleic acid sequence selected from any of:
  - (a) SEQ ID Nos: 2 to 13;
  - (b) a sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 2 to 13;
  - (c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and
  - (d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to any one of the polypeptides encoded by SEQ ID Nos: 2 to 13.
3. (Amended) A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 1.
4. (Amended) A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and a second polypeptide.
5. (Amended) The nucleic acid molecule of claim 4 wherein the second polypeptide is a heterologous signal peptide.
6. (Amended) The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.
7. (Amended) A nucleic acid molecule according to claim 1, operatively linked to one or more expression control sequences.
8. (Amended) A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:
  - (i) SEQ ID Nos: 1 to 13;



- 00000007-100401
- (ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);
  - (iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;
  - (vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and
  - (vii) a nucleic acid sequence which encodes a polypeptide as defined in (i) to (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed.

9. (Amended) A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

- (a) a first polypeptide selected from any of:
  - (i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;
  - (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;
  - (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and
  - (vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence

to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

10. (Amended) The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

11. (Amended) The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

12. (Amended) The vaccine of any one of claim 8 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

13. (Amended) A vaccine according to claim 8 wherein each first nucleic acid is expressed as a polypeptide, and wherein the vaccine comprises a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

14. (Amended) The vaccine according to claim 13 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

15. (Amended) A pharmaceutical composition comprising a nucleic acid according to claim 1 and a pharmaceutically acceptable carrier.

16. (Amended) A pharmaceutical composition comprising a vaccine according to claim 8 and a pharmaceutically acceptable carrier.

17. (Amended) A unicellular host transformed with the nucleic acid molecule of claim 7.

18. (Amended) An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. (Amended) An isolated primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

20. (Amended) A polypeptide encoded by a nucleic acid sequence according to claim 2.

21. (Amended) A polypeptide comprising an amino acid sequence selected from any one of:

- (a) SEQ ID Nos: 15 to 26;
- (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

22. (Amended) A fusion protein comprising a polypeptide of claim 21 and a second polypeptide.

23. (Amended) The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. (Amended) The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

25. (Amended) A method for producing a polypeptide of claim 21, comprising the step of culturing a unicellular host transformed with a nucleic acid encoding a polypeptide of claim 21.

26. (Amended) An antibody against the polypeptide of claim 21.

27. (Amended) A vaccine comprising at least one first polypeptide selected from any one of:
- (i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;
  - (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;
  - (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and
  - (vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v).

28. (Amended) A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

- (a) a first polypeptide selected from any of:
  - (i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;
  - (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
  - (iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;
  - (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and
  - (vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide.

29. (Amended) The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. (Amended) The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

31. (Amended) A vaccine comprising at least one first polypeptide according to claim 20 and an additional polypeptide which enhances the immune response to the first polypeptide.

32. (Amended) The vaccine of claim 31 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

33. (Amended) A pharmaceutical composition comprising a polypeptide according to claim 20 and a pharmaceutically acceptable carrier.

34. (Amended) A pharmaceutical composition comprising a vaccine according to claim 27 and a pharmaceutically acceptable carrier.

35. (Amended) A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

36. (Amended) A method for preventing or treating *Chlamydia* infection comprising administering to a patient an effective amount of:

(a) a nucleic acid according to claim 2;

(b) a vaccine comprising a vaccine vector and at least one first nucleic acid according to claim 2;

(c) a pharmaceutical composition comprising a nucleic acid according to claim 2 and a pharmaceutically acceptable carrier;

(d) a polypeptide encoded by a nucleic acid according to claim 2; or

(e) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

37. (Amended) A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

(a) a nucleic acid according to claim 2;

(b) a polypeptide encoded by a nucleic acid according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

38. (Amended) A diagnostic kit comprising instructions for use and a component selected from any one of:

(a) a nucleic acid according to claim 2;

(b) a polypeptide encoded by a nucleic acid according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

39. (Amended) A method for identifying a polypeptide of claim 20 which induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide of claim 20; and

(b) inoculating the immunized mouse with *Chlamydia*;

wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

REMARKS

Applicant respectfully requests that the foregoing amendments to the claims be entered in order to avoid this application incurring a surcharge for the presence of one or more multiple dependent claims and to improve clarity.

Respectfully submitted,

Date: June 22, 2001

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032931-0253-0001

MARKED UP CLAIMS

1. A nucleic acid molecule comprising a nucleic acid  
sequence which encodes a polypeptide selected from any one  
of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12  
consecutive amino acids from a polypeptide of (a);  
and

(c) a polypeptide of (a) or (b) which has been modified  
without loss of immunogenicity, wherein said modified  
polypeptide is at least 75% identical in amino acid  
sequence to the corresponding polypeptide of (a) or  
(b).

2. A nucleic acid molecule comprising a nucleic acid  
sequence selected from any of:

(a) SEQ ID Nos: 2 to 13;

(b) a sequence which encodes a polypeptide encoded by any  
one of SEQ ID Nos: 2 to 13;

(c) a sequence comprising at least 38 consecutive  
nucleotides from any one of the nucleic acid  
sequences of (a) and (b); and

(d) a sequence which encodes a polypeptide which is at  
least 75% identical in amino acid sequence to any one  
of the polypeptides encoded by SEQ ID Nos: 2 to 13.

3. A nucleic acid molecule comprising a nucleic acid  
sequence which is anti-sense to the nucleic acid molecule of  
claim 1 ~~or~~ 2.

4. A nucleic acid molecule comprising a nucleic acid  
sequence which encodes a fusion protein, said fusion protein  
comprising a polypeptide encoded by a nucleic acid molecule  
according to claim 1 and a second polypeptide.



5. The nucleic acid molecule of claim 4 wherein the second polypeptide is a heterologous signal peptide.

6. The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.

7. A nucleic acid molecule according to ~~any one of~~  
10 ~~claims 1 to 6,~~claim 1, operatively linked to one or more expression control sequences.

8. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

- 15 (i) SEQ ID Nos: 1 to 13;
- (ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
- (iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid
- 20 sequences of (i) and (ii);
- (iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
- (v) a nucleic acid sequence which encodes a polypeptide
- 25 whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;
- (vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and
- (vii) a nucleic acid sequence which encodes a polypeptide
- 30 as defined in (i) to (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (v) or the corresponding fragment of
- 35 (vi);

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune-expressed.

5 response to the polypeptide expressed by the first nucleic acid.

9. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune-expressed.

~~response to the first polypeptide.~~

10. The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

11. The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

12. The vaccine of any one of ~~claims 8 to 11~~ wherein claim 8 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

13. A vaccine ~~comprising at least one first nucleic acid according to any one of claims 1, 2, and 4 to 7 and a vaccine vector~~ claim 8 wherein each first nucleic acid is expressed as a polypeptide, and wherein the vaccine ~~optionally comprising~~ comprises a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by ~~said~~ the first nucleic acid.

14. The vaccine ~~of any one of claims 8 to~~ according to claim 13 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

15. A pharmaceutical composition comprising a nucleic acid according to ~~any one of claims 1 to 7~~ claim 1 and a pharmaceutically acceptable carrier.

16. A pharmaceutical composition comprising a vaccine according to ~~any one of claims 8 to 14~~ claim 8 and a pharmaceutically acceptable carrier.

17. A unicellular host transformed with the nucleic acid molecule of claim 7.

18. An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. An isolated primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

20. A polypeptide encoded by a nucleic acid sequence according to ~~any one of claims 1, 2 and 4 to 7.~~claim 2.

21. A polypeptide comprising an amino acid sequence selected from any one of:

- (a) SEQ ID Nos: 15 to 26;
- (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

22. A fusion protein comprising a polypeptide of claim 20 or 21 and a second polypeptide.

23. The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

25. A method for producing a polypeptide of claim ~~20 or~~  
21, ~~or a fusion protein of any one of claims 22 to 24,~~  
comprising the step of culturing a unicellular host transformed  
with a nucleic acid encoding a polypeptide of claim ~~17-21.~~

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26. An antibody against the polypeptide of claim ~~20 or~~  
21, ~~or against a fusion protein of any one of claims 22 to~~  
~~24, 21.~~

10 27. A vaccine comprising at least one first polypeptide  
selected from any one of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to  
13;

(ii) a polypeptide encoded by a nucleic acid sequence  
15 comprising at least 38 consecutive nucleotides from any one of  
SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in  
amino acid sequence to the polypeptide encoded by any one of  
SEQ ID Nos: 1 to 13;

20 (iv) a polypeptide whose sequence is set forth in any one  
of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12  
consecutive amino acids from any one of SEQ ID Nos: 14 to 26;  
and

25 (vi) a polypeptide as defined in (i) to (iv) or an  
immunogenic fragment as defined in (v) which has been modified  
without loss of immunogenicity, wherein said modified  
polypeptide or fragment is at least 75% identical in amino acid  
sequence to the corresponding polypeptide of (i) to (iv) or the  
30 corresponding fragment of ~~(v)~~ (v).

~~wherein the vaccine optionally comprises an additional~~  
~~polypeptide which enhances the immune response to the first~~  
~~polypeptide.~~

28. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

~~(iii)~~ a (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

~~wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.~~

29. The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

31. A vaccine comprising at least one first polypeptide according to ~~any one of claims 20 to 24, optionally~~

~~comprising claim 20 and~~ an additional polypeptide which enhances the immune response to the first polypeptide.

32. The vaccine of ~~any one of claims 27 to~~ claim 31

5 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

33. A pharmaceutical composition comprising a polypeptide according to ~~any one of claims~~ claim 20 to 24 and a

10 pharmaceutically acceptable carrier.

34. A pharmaceutical composition comprising a vaccine according to ~~any one of claims~~ claim 27 to 32 and a pharmaceutically acceptable carrier.

15 35. A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

20 36. A method for preventing or treating *Chlamydia* infection ~~using~~ comprising administering to a patient an effective amount of:

~~(a) the nucleic acid of any one of claims 1 to 7;~~  
~~(b) the vaccine of any one of claims 8 to 14 and 27 to 32;~~ (a)  
25 a nucleic acid according to claim 2;

(b) a vaccine comprising a vaccine vector and at least one first nucleic acid according to claim 2;

~~(c) the~~ (c) a pharmaceutical composition of any one of claims 15, 16 and 33 to 35, comprising a nucleic acid according to claim 2 and a pharmaceutically acceptable carrier;

30 ~~(d) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; or~~

~~(e) the antibody of claim 26. (d) a polypeptide encoded by a nucleic acid according to claim 2; or~~

~~(e) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.~~

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37. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

~~(a) the nucleic acid of any one of claims 1 to 7;~~

10 ~~(b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and~~

~~(c) the antibody of claim 26.~~

~~(a) a nucleic acid according to claim 2;~~

15 ~~(b) a polypeptide encoded by a nucleic acid according to claim 2; and~~

~~(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.~~

38. A diagnostic kit comprising instructions for use and a component selected from any one of:

20 ~~(a) the nucleic acid of any one of claims 1 to 7;~~

~~(b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and~~

~~(c) the antibody of claim 26.~~

~~(a) a nucleic acid according to claim 2;~~

25 ~~(b) a polypeptide encoded by a nucleic acid according to claim 2; and~~

~~(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.~~

39. A method for identifying a polypeptide of claim 20 ~~or 21, or a fusion protein of any one of claims 22 to 24 which~~

30



induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

5 (a) immunizing a mouse with the polypeptide ~~or fusion~~  
~~protein;~~ of claim 20; and

(b) inoculating the immunized mouse with *Chlamydia*; wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

TITLE OF INVENTION

CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF

5 REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of 13 U.S. provisional applications: U.S. Provisional Application Nos. 60/113,280, 60/113,281, 60/113,282, 60/113,283, 60/113,284, 60/113,285, 60/113,385, all of which were filed December 23, 10 1998; and U.S. Provisional Application Nos. 60/114,050, 60/114,056, 60/114,057, 60/114,058, 60/114,059, 60/114,061, all of which were filed December 28, 1998.

FIELD OF INVENTION

15 The present invention relates to *Chlamydia* antigens and corresponding DNA molecules, which can be used to prevent and treat *Chlamydia* infection in mammals, such as humans.

BACKGROUND OF THE INVENTION

20 *Chlamydiae* are prokaryotes. They exhibit morphologic and structural similarities to gram-negative bacteria including a trilaminar outer membrane, which contains lipopolysaccharide and several membrane proteins that are structurally and functionally analogous to proteins found in *E coli*. They are 25 obligate intra-cellular parasites with a unique biphasic life cycle consisting of a metabolically inactive but infectious extracellular stage and a replicating but non-infectious intracellular stage. The replicative stage of the life-cycle takes place within a membrane-bound inclusion which sequesters 30 the bacteria away from the cytoplasm of the infected host cell.

*C. pneumoniae* is a common human pathogen, originally described as the TWAR strain of *Chlamydia psittaci* but subsequently recognised to be a new species. *C. pneumoniae* is antigenically, genetically and morphologically distinct from

other chlamydia species (*C. trachomatis*, *C. pecorum* and *C. psittaci*). It shows 10% or less DNA sequence homology with either of *C. trachomatis* or *C. psittaci*.

*C. pneumoniae* is a common cause of community acquired pneumonia, only less frequent than *Streptococcus pneumoniae* and *Mycoplasma pneumoniae* (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477). It can also cause upper respiratory tract symptoms and disease, including bronchitis and sinusitis (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Grayston et al (1990) Journal of Infectious Diseases 161:618; Marrie (1993) Clinical Infectious Diseases. 18:501; Wang et al (1986) Chlamydial infections. Cambridge University Press, Cambridge. p. 329. The great majority of the adult population (over 60%) has antibodies to *C. pneumoniae* (Wang et al (1986) Chlamydial infections. Cambridge University Press, Cambridge. p. 329), indicating past infection which was unrecognized or asymptomatic.

*C. pneumoniae* infection usually presents as an acute respiratory disease (i.e., cough, sore throat, hoarseness, and fever; abnormal chest sounds on auscultation). For most patients, the cough persists for 2 to 6 weeks, and recovery is slow. In approximately 10% of these cases, upper respiratory tract infection is followed by bronchitis or pneumonia. Furthermore, during a *C. pneumoniae* epidemic, subsequent co-infection with pneumococcus has been noted in about half of these pneumonia patients, particularly in the infirm and the elderly. As noted above, there is more and more evidence that *C. pneumoniae* infection is also linked to diseases other than respiratory infections.

The reservoir for the organism is presumably people. In contrast to *C. psittaci* infections, there is no known bird or animal reservoir. Transmission has not been clearly defined.

It may result from direct contact with secretions, from fomites, or from airborne spread. There is a long incubation period, which may last for many months. Based on analysis of epidemics, *C. pneumoniae* appears to spread slowly through a population (case-to-case interval averaging 30 days) because infected persons are inefficient transmitters of the organism. Susceptibility to *C. pneumoniae* is universal. Reinfections occur during adulthood, following the primary infection as a child. *C. pneumoniae* appears to be an endemic disease throughout the world, noteworthy for superimposed intervals of increased incidence (epidemics) that persist for 2 to 3 years. *C. trachomatis* infection does not confer cross-immunity to *C. pneumoniae*. Infections are easily treated with oral antibiotics, tetracycline or erythromycin (2 g/d, for at least 10 to 14 d). A recently developed drug, azithromycin, is highly effective as a single-dose therapy against chlamydial infections.

In most instances, *C. pneumoniae* infection is often mild and without complications, and up to 90% of infections are subacute or unrecognized. Among children in industrialized countries, infections have been thought to be rare up to the age of 5 y, although a recent study (E Normann et al, Chlamydia pneumoniae in children with acute respiratory tract infections, Acta Paediatrica, 1998, Vol 87, Iss 1, pp 23-27) has reported that many children in this age group show PCR evidence of infection despite being seronegative, and estimates a prevalence of 17-19% in 2-4 y olds. In developing countries, the seroprevalence of *C. pneumoniae* antibodies among young children is elevated, and there are suspicions that *C. pneumoniae* may be an important cause of acute lower respiratory tract disease and mortality for infants and children in tropical regions of the world.

From seroprevalence studies and studies of local epidemics, the initial *C. pneumoniae* infection usually happens

between the ages of 5 and 20 y. In the USA, for example, there are estimated to be 30,000 cases of childhood pneumonia each year caused by *C. pneumoniae*. Infections may cluster among groups of children or young adults (e.g., school pupils or military conscripts).

*C. pneumoniae* causes 10 to 25% of community-acquired lower respiratory tract infections (as reported from Sweden, Italy, Finland, and the USA). During an epidemic, *C. pneumoniae* infection may account for 50 to 60% of the cases of pneumonia. During these periods, also, more episodes of mixed infections with *S. pneumoniae* have been reported.

Reinfection during adulthood is common; the clinical presentation tends to be milder. Based on population seroprevalence studies, there tends to be increased exposure with age, which is particularly evident among men. Some investigators have speculated that a persistent, asymptomatic *C. pneumoniae* infection state is common.

In adults of middle age or older, *C. pneumoniae* infection may progress to chronic bronchitis and sinusitis. A study in the USA revealed that the incidence of pneumonia caused by *C. pneumoniae* in persons younger than 60 years is 1 case per 1,000 persons per year; but in the elderly, the disease incidence rose three-fold. *C. pneumoniae* infection rarely leads to hospitalization, except in patients with an underlying illness.

Of considerable importance is the association of atherosclerosis and *C. pneumoniae* infection. There are several epidemiological studies showing a correlation of previous infections with *C. pneumoniae* and heart attacks, coronary artery and carotid artery disease (Saikku et al. (1988) Lancet; ii:983; Thom et al. (1992) JAMA 268:68; Linnanmaki et al. (1993), Circulation 87:1030; Saikku et al. (1992) Annals Internal Medicine 116:273; Melnick et al (1993) American Journal of Medicine 95:499). Moreover, the organisms have been detected in

atheromas and fatty streaks of the coronary, carotid, peripheral arteries and aorta (Shor et al. (1992) South African. Medical Journal 82:158; Kuo et al. (1993) Journal of Infectious Diseases 167:841; Kuo et al. (1993) Arteriosclerosis and Thrombosis 13:1500; Campbell et al (1995) Journal of Infectious Diseases 172:585; Chiu et al. Circulation, 1997 (In Press)). Viable *C. pneumoniae* has been recovered from the coronary and carotid artery (Ramirez et al (1996) Annals of Internal Medicine 125:979; Jackson et al. Abst. K121, p272, 36<sup>th</sup> ICAAC, 15-18 Sept. 1996, New Orleans). Furthermore, it has been shown that *C. pneumoniae* can induce changes of atherosclerosis in a rabbit model (Fong et al (1997) Journal of Clinical Microbiology 35:48). Taken together, these results indicate that it is highly probable that *C. pneumoniae* can cause atherosclerosis in humans, though the epidemiological importance of chlamydial atherosclerosis remains to be demonstrated.

A number of recent studies have also indicated an association between *C. pneumoniae* infection and asthma. Infection has been linked to wheezing, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults, and small-scale studies have shown that prolonged antibiotic treatment was effective at greatly reducing the severity of the disease in some individuals (Hahn DL, et al. Evidence for Chlamydia pneumoniae infection in steroid-dependent asthma. Ann Allergy Asthma Immunol. 1998 Jan; 80(1): 45-49; Hahn DL, et al. Association of Chlamydia pneumoniae IgA antibodies with recently symptomatic asthma. Epidemiol Infect. 1996 Dec; 117(3): 513-517; Bjornsson E, et al. Serology of chlamydia in relation to asthma and bronchial hyperresponsiveness. Scand J Infect Dis. 1996; 28(1): 63-69; Hahn DL. Treatment of Chlamydia pneumoniae infection in adult asthma: a before-after trial. J Fam Pract. 1995 Oct; 41(4): 345-351; Allegra L, et al. Acute exacerbations of asthma in adults: role of Chlamydia pneumoniae infection. Eur Respir J. 1994 Dec; 7(12): 2165-2168; Hahn DL,

et al. Association of Chlamydia pneumoniae (strain TWAR) infection with wheezing, asthmatic bronchitis, and adult-onset asthma. JAMA. 1991 Jul 10; 266(2): 225-230).

- In light of these results a protective vaccine against
- 5 C. pneumoniae infection would be of considerable importance. There is not yet an effective vaccine for any human chlamydial infection. It is conceivable that an effective vaccine can be developed using physically or chemically inactivated Chlamydiae. However, such a vaccine does not have a high margin of safety.
- 10 In general, safer vaccines are made by genetically manipulating the organism by attenuation or by recombinant means. Accordingly, a major obstacle in creating an effective and safe vaccine against human chlamydial infection has been the paucity of genetic information regarding Chlamydia, specifically
- 15 C. pneumoniae.

- Studies with C. trachomatis and C. psittaci indicate that safe and effective vaccine against Chlamydia is an attainable goal. For example, mice which have recovered from a lung infection with C. trachomatis are protected from
- 20 infertility induced by a subsequent vaginal challenge (Pal et al.(1996) Infection and Immunity.64:5341). Similarly, sheep immunized with inactivated C. psittaci were protected from subsequent chlamydial-induced abortions and stillbirths (Jones et al. (1995) Vaccine 13:715). Protection from chlamydial
- 25 infections has been associated with Th1 immune responses, particularly the induction of INF $\gamma$  - producing CD4+T-cells (Igietsemes et al. (1993) Immunology 5:317). The adoptive transfer of CD4+ cell lines or clones to nude or SCID mice conferred protection from challenge or cleared chronic disease
- 30 (Igietseme et al (1993) Regional Immunology 5:317; Magee et al (1993) Regional Immunology 5: 305), and in vivo depletion of CD4+ T cells exacerbated disease post-challenge (Landers et al (1991) Infection & Immunity 59:3774; Magee et al (1995) Infection & Immunity 63:516). However, the presence of

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sufficiently high titres of neutralising antibody at mucosal surfaces can also exert a protective effect (Cotter et al. (1995) Infection and Immunity 63:4704).

Antigenic variation within the species *C. pneumoniae* is not well documented due to insufficient genetic information, though variation is expected to exist based on *C. trachomatis*. Serovars of *C. trachomatis* are defined on the basis of antigenic variation in the major outer membrane protein (MOMP), but published *C. pneumoniae* MOMP gene sequences show no variation between several diverse isolates of the organism (Campbell et al (1990) Infection and Immunity 58:93; McCafferty et al (1995) Infection and Immunity 63:2387-9; Gaydos et al (1992) Infection and Immunity 60(12):5319-5323). Regions of the protein known to be conserved in other chlamydial MOMP are conserved in *C. pneumoniae* (Campbell et al (1990) Infection and Immunity 58:93; McCafferty et al (1995) Infection and Immunity 63:2387-9). One study has described a strain of *C. pneumoniae* with a MOMP of greater than usual molecular weight, but the gene for this has not been sequenced (Grayston et al. (1995) Journal of Infectious Diseases 168:1231). Partial sequences of outer membrane protein 2 from nine diverse isolates were also found to be invariant (Ramirez et al (1996) Annals of Internal Medicine 125:979). The genes for HSP60 and HSP70 show little variation from other chlamydial species, as would be expected. The gene encoding a 76kDa antigen has been cloned from a single strain of *C. pneumoniae*. It has no significant similarity with other known chlamydial genes (Marrie (1993) Clinical Infectious Diseases. 18:501).

Many antigens recognised by immune sera to *C. pneumoniae* are conserved across all chlamydiae, but 98kDa, 76 kDa and 54 kDa proteins appear to be *C. pneumoniae*-specific (Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477; Marrie (1993) Clinical Infectious Diseases. 18:501; Wiedmann-Al-Ahmad M, et al. Reactions of polyclonal and



neutralizing anti-p54 monoclonal antibodies with an isolated, species-specific 54-kilodalton protein of *Chlamydia pneumoniae*. Clin Diagn Lab Immunol. 1997 Nov; 4(6): 700-704).

Immunoblotting of isolates with sera from patients does show variation of blotting patterns between isolates, indicating that serotypes *C. pneumoniae* may exist (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Ramirez et al (1996) Annals of Internal Medicine 125:979). However, the results are potentially confounded by the infection status of the patients, since immunoblot profiles of a patient's sera change with time post-infection. An assessment of the number and relative frequency of any serotypes, and the defining antigens, is not yet possible.

Accordingly, a need exists for identifying and isolating polynucleotide sequences of *C. pneumoniae* for use in preventing and treating *Chlamydia* infection.

#### SUMMARY OF THE INVENTION

The present invention provides purified and isolated polynucleotide molecules that encode *Chlamydia* polypeptides which can be used in methods to prevent, treat, and diagnose *Chlamydia* infection. In one form of the invention, the polynucleotide molecules are selected from DNA that encode polypeptides CPN100686 RY 54 (SEQ ID No: 1), CPN100696 RY-55 (SEQ ID No: 2), CPN100709 RY-57 (SEQ ID No: 3), CPN100710 RY-58 (SEQ ID No:4), CPN100711 RY-59 (SEQ ID No: 5), CPN100877 RY-61 (SEQ ID No:6), CPN100325 RY-62 (SEQ ID No:7), CPN100368 RY-63 (SEQ ID No:8), CPN100624 RY-64 (SEQ ID No:9), CPN100633 RY-65 (SEQ ID No:10), CPN100985 RY-66 (SEQ ID No:11), CPN100987 RY-67 (SEQ ID No:12) and CPN100988 RY-68 (SEQ ID No:13). Another form of the invention provides polypeptides corresponding to the isolated DNA molecules. The amino acid sequences of the corresponding encoded polypeptides are shown for CPN100686 RY 54 as SEQ ID No: 14, CPN100696 RY-55 as SEQ ID No: 15, CPN100709 RY-57 as SEQ ID

No: 16, CPN100710 RY-58 as SEQ ID No: 17, CPN100711 RY-59 as SEQ ID No: 18, CPN100877 RY-61 as SEQ ID No: 19, CPN100325 RY-62 as SEQ ID No: 20, CPN100368 RY-63 as SEQ ID No: 21, CPN100624 RY-64 as SEQ ID No: 22, CPN100633 RY-65 as SEQ ID No: 23, CPN100985 RY-66 as SEQ ID No: 24, CPN100987 RY-67 as SEQ ID No: 24 and CPN100988 RY-68 as SEQ ID No: 26.

Those skilled in the art will readily understand that the invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, also provides polynucleotides encoding 10 fragments derived from such peptides. Moreover, the invention is understood to provide mutants and derivatives of such polypeptides and fragments derived therefrom, which result from the addition, deletion, or substitution of non-essential amino acids as described herein. Those skilled in the art would also 15 readily understand that the invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, further provides monospecific antibodies that specifically bind to such polypeptides.

The present invention has wide application and includes 20 expression cassettes, vectors, and cells transformed or transfected with the polynucleotides of the invention. Accordingly, the present invention further provides (i) a method for producing a polypeptide of the invention in a recombinant host system and related expression cassettes, vectors, and 25 transformed or transfected cells; (ii) a vaccine, or a live vaccine vector such as a pox virus, *Salmonella typhimurium*, or *Vibrio cholerae* vector, containing a polynucleotide of the invention, such vaccines and vaccine vectors being useful for, e.g., preventing and treating *Chlamydia* infection, in 30 combination with a diluent or carrier, and related pharmaceutical compositions and associated therapeutic and/or prophylactic methods; (iii) a therapeutic and/or prophylactic use of an RNA or DNA molecule of the invention, either in a naked form or formulated with a delivery vehicle, a polypeptide

or combination of polypeptides, or a monospecific antibody of the invention, and related pharmaceutical compositions; (iv) a method for diagnosing the presence of *Chlamydia* in a biological sample, which can involve the use of a DNA or RNA molecule, a monospecific antibody, or a polypeptide of the invention; and (v) a method for purifying a polypeptide of the invention by antibody-based affinity chromatography.

#### BRIEF DESCRIPTION OF THE DRAWINGS

The present invention will be further understood from the following description with reference to the drawings, in which:

Figure 1 through 13 show the restriction enzyme analysis of the nucleic acid sequences of the invention.

Figures 14 through 26 show an identification of T and B cell epitopes from the amino acid sequences SEQ ID Nos: 14 to 26.

#### DETAILED DESCRIPTION OF INVENTION

Open reading frames (ORFs) encoding chlamydial polypeptides have been identified from the *C. pneumoniae* genome. These polypeptides include polypeptides found permanently in the bacterial membrane structure, polypeptides present in the external vicinity of the bacterial membrane, polypeptides found permanently in the inclusion membrane structure, polypeptides present in the external vicinity of the inclusion membrane, and polypeptides released into the cytoplasm of the infected cell. These polypeptides can be used to prevent and treat *Chlamydia* infection.

The polypeptide CPN100686 RY 54 whose amino acid sequence is shown as SEQ ID No: 14 is a putative 98 kDa outer membrane protein; the polypeptide CPN100696 RY-55 (SEQ ID No: 15) is consistent with a sulfur-rich protein; the polypeptide CPN100709 RY-57 (SEQ ID No: 16) is a ABC transporter; the polypeptide CPN100710 RY-58 (SEQ ID No: 17) is an adhesion

protein; the polypeptide CPN100711 RY-59 (SEQ ID No: 18) is a putative outer membrane protein; the polypeptide CPN100877 RY-61 (SEQ ID No: 19) is a putative 98 kDa outer membrane protein, and so are the polypeptides CPN100325 RY-62 (SEQ ID No: 20),  
5 CPN100368 RY-63 (SEQ ID No: 21), CPN100624 RY-64 (SEQ ID No: 22), and CPN100633 RY-65 (SEQ ID No: 23); the polypeptide CPN100985 RY-66 (SEQ ID No: 24) is yscT; and CPN100988 RY-68 (SEQ ID No: 26) is a flagellar protein.

According to a first aspect of the invention, isolated  
10 polynucleotides are provided which encode the precursor and mature forms of *Chlamydia* polypeptides, whose amino acid sequences are selected from the group consisting of SEQ ID Nos: 14 to 26.

The term "isolated polynucleotide" is defined as a  
15 polynucleotide removed from the environment in which it naturally occurs. For example, a naturally-occurring DNA molecule present in the genome of a living bacteria or as part of a gene bank is not isolated, but the same molecule separated from the remaining part of the bacterial genome, as a result of,  
20 e.g., a cloning event (amplification), is isolated. Typically, an isolated DNA molecule is free from DNA regions (e.g., coding regions) with which it is immediately contiguous at the 5' or 3' end, in the naturally occurring genome. Such isolated polynucleotides may be part of a vector or a composition and  
25 still be defined as isolated in that such a vector or composition is not part of the natural environment of such polynucleotide.

The polynucleotides of the invention are either RNA or DNA (cDNA, genomic DNA, or synthetic DNA), or modifications,  
30 variants, homologs or fragments thereof. The DNA is either double-stranded or single-stranded, and, if single-stranded, is either the coding strand or the non-coding (anti-sense) strand. Any one of the sequences that encode the polypeptides of the invention as shown in SEQ ID Nos: 1 to 13 is (a) a coding

sequence, (b) a ribonucleotide sequence derived from transcription of (a), or (c) a coding sequence which uses the redundancy or degeneracy of the genetic code to encode the same polypeptides. By "polypeptide" or "protein" is meant any chain of amino acids, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation). Both terms are used interchangeably in the present application.

Consistent with the first aspect of the invention, amino acid sequences are provided which are homologous to any one of SEQ ID Nos: 14 to 26. As used herein, "homologous amino acid sequence" is any polypeptide which is encoded, in whole or in part, by a nucleic acid sequence which hybridizes at 25-35°C below critical melting temperature ( $T_m$ ), to any portion of the nucleic acid sequences of SEQ ID Nos: 1 to 13. A homologous amino acid sequence is one that differs from an amino acid sequence shown in any one of SEQ ID Nos: 13 to 26 by one or more conservative amino acid substitutions. Such a sequence also encompass serotypic variants (defined below) as well as sequences containing deletions or insertions which retain inherent characteristics of the polypeptide such as immunogenicity. Preferably, such a sequence is at least 75%, more preferably 80%, and most preferably 90% identical to any one of SEQ ID Nos: 14 to 26.

Homologous amino acid sequences include sequences that are identical or substantially identical to SEQ ID Nos: 14 to 26. By "amino acid sequence substantially identical" is meant a sequence that is at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to an amino acid sequence of reference and that preferably differs from the sequence of reference by a majority of conservative amino acid substitutions.

Conservative amino acid substitutions are substitutions among amino acids of the same class. These classes include, for example, amino acids having uncharged polar side chains, such as

asparagine, glutamine, serine, threonine, and tyrosine; amino acids having basic side chains, such as lysine, arginine, and histidine; amino acids having acidic side chains, such as aspartic acid and glutamic acid; and amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Homology is measured using sequence analysis software such as Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705. Amino acid sequences are aligned to maximize identity. Gaps may be artificially introduced into the sequence to attain proper alignment. Once the optimal alignment has been set up, the degree of homology is established by recording all of the positions in which the amino acids of both sequences are identical, relative to the total number of positions.

Homologous polynucleotide sequences are defined in a similar way. Preferably, a homologous sequence is one that is at least 45%, more preferably 60%, and most preferably 85% identical to any one of coding sequences SEQ ID Nos: 1 to 13.

Consistent with the first aspect of the invention, polypeptides having a sequence homologous to any one of SEQ ID Nos: 14 to 26 include naturally-occurring allelic variants, as well as mutants or any other non-naturally occurring variants that retain the inherent characteristics of the polypeptide of SEQ ID Nos: 14 to 26.

As is known in the art, an allelic variant is an alternate form of a polypeptide that is characterized as having a substitution, deletion, or addition of one or more amino acids that does not alter the biological function of the polypeptide. By "biological function" is meant the function of the polypeptide in the cells in which it naturally occurs, even if the function is not necessary for the growth or survival of the

cells. For example, the biological function of a porin is to allow the entry into cells of compounds present in the extracellular medium. Biological function is distinct from antigenic property. A polypeptide can have more than one biological function.

Allelic variants are very common in nature. For example, a bacterial species such as *C. pneumoniae*, is usually represented by a variety of strains that differ from each other by minor allelic variations. Indeed, a polypeptide that fulfills the same biological function in different strains can have an amino acid sequence (and polynucleotide sequence) that is not identical in each of the strains. Despite this variation, an immune response directed generally against many allelic variants has been demonstrated. In studies of the *Chlamydial* MOMP antigen, cross-strain antibody binding plus neutralization of infectivity occurs despite amino acid sequence variation of MOMP from strain to strain, indicating that the MOMP, when used as an immunogen, is tolerant of amino acid variations.

Polynucleotides encoding homologous polypeptides or allelic variants are retrieved by polymerase chain reaction (PCR) amplification of genomic bacterial DNA extracted by conventional methods. This involves the use of synthetic oligonucleotide primers matching upstream and downstream of the 5' and 3' ends of the encoding domain. Suitable primers are designed according to the nucleotide sequence information provided in SEQ ID Nos: 1 to 13. The procedure is as follows: a primer is selected which consists of 10 to 40, preferably 15 to 25 nucleotides. It is advantageous to select primers containing C and G nucleotides in a proportion sufficient to ensure efficient hybridization; i.e., an amount of C and G nucleotides of at least 40%, preferably 50% of the total nucleotide content. A standard PCR reaction contains typically 0.5 to 5 Units of Taq DNA polymerase per 100  $\mu$ L, 20 to 200  $\mu$ M deoxynucleotide each,

preferably at equivalent concentrations, 0.5 to 2.5 MM magnesium over the total deoxynucleotide concentration,  $10^5$  to  $10^6$  target molecules, and about 20 pmol of each primer. About 25 to 50 PCR cycles are performed, with an annealing temperature  $15^\circ\text{C}$  to  $5^\circ\text{C}$  below the true  $T_m$  of the primers. A more stringent annealing temperature improves discrimination against incorrectly annealed primers and reduces incorporation of incorrect nucleotides at the 3' end of primers. A denaturation temperature of  $95^\circ\text{C}$  to  $97^\circ\text{C}$  is typical, although higher temperatures may be appropriate for denaturation of G+C-rich targets. The number of cycles performed depends on the starting concentration of target molecules, though typically more than 40 cycles is not recommended as non-specific background products tend to accumulate.

An alternative method for retrieving polynucleotides encoding homologous polypeptides or allelic variants is by hybridization screening of a DNA or RNA library. Hybridization procedures are well-known in the art and are described in Ausubel et al., (Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994), Silhavy et al. (Silhavy et al. Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, 1984), and Davis et al. (Davis et al. A Manual for Genetic Engineering: Advanced Bacterial Genetics, Cold Spring Harbor Laboratory Press, 1980)). Important parameters for optimizing hybridization conditions are reflected in a formula used to obtain the critical melting temperature above which two complementary DNA strands separate from each other (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539). For polynucleotides of about 600 nucleotides or larger, this formula is as follows:  $T_m = 81.5 + 0.5 \times (\% \text{ G+C}) + 1.6 \log (\text{positive ion concentration}) - 0.6 \times (\% \text{ formamide})$ . Under appropriate stringency conditions, hybridization temperature ( $T_h$ ) is approximately 20 to  $40^\circ\text{C}$ , 20 to  $25^\circ\text{C}$ , or, preferably 30 to  $40^\circ\text{C}$ .



below the calculated  $T_m$ . Those skilled in the art will understand that optimal temperature and salt conditions can be readily determined.

For the polynucleotides of the invention, stringent conditions are achieved for both pre-hybridizing and hybridizing incubations (i) within 4-16 hours at 42°C, in 6 x SSC containing 50% formamide, or (ii) within 4-16 hours at 65°C in an aqueous 6 x SSC solution (1 M NaCl, 0.1 M sodium citrate (pH 7.0)).

Useful homologs and fragments thereof that do not occur naturally are designed using known methods for identifying regions of an antigen that are likely to tolerate amino acid sequence changes and/or deletions. As an example, homologous polypeptides from different species are compared; conserved sequences are identified. The more divergent sequences are the most likely to tolerate sequence changes. Homology among sequences may be analyzed using the BLAST homology searching algorithm of Altschul et al., Nucleic Acids Res.25:3389-3402 (1997). Alternatively, sequences are modified such that they become more reactive to T- and/or B-cells. (See Figures 11 to 15 below for identification of T- and B- epitopes). Yet another alternative is to mutate a particular amino acid residue or sequence within the polypeptide *in vitro*, then screen the mutant polypeptides for their ability to prevent or treat Chlamydia infection according to the method outlined below.

A person skilled in the art will readily understand that by following the screening process of this invention, it will be determined without undue experimentation whether a particular homolog of any of SEQ ID Nos: 14 to 26 may be useful in the prevention or treatment of Chlamydia infection. The screening procedure comprises the steps:

- (i) immunizing an animal, preferably mouse, with the test homolog or fragment;
- (ii) inoculating the immunized animal with Chlamydia; and,

- (iii) selecting those homologs or fragments which confer protection against Chlamydia.

By "conferring protection" is meant that there is a reduction in severity of any of the effects of Chlamydia infection, in comparison with a control animal which was not immunized with the test homolog or fragment.

It has been previously demonstrated (Yang, Z. P., Chi, E. Y., Kuo, C. C. and Grayston, J. T. 1993. A mouse model of *C. pneumoniae* strain TWAR pneumonitis. 61(5):2037-2040) that 10 mice are susceptible to intranasal infection with different isolates of *C. pneumoniae*. Strain AR-39 (Chi, E. Y., Kuo, C. C. and Grayston, J. T., 1987. Unique ultrastructure in the elementary body of Chlamydia sp. strain TWAR. J. Bacteriol. 169(8):3757-63) was used in Balb/c mice as a challenge infection 15 model to examine the capacity of chlamydia gene products delivered as naked DNA to elicit a protective response against a sublethal *C. pneumoniae* lung infection. Protective immunity is defined as an accelerated clearance of pulmonary infection.

Groups of 7 to 9 week old male Balb/c mice (6 to 10 per 20 group) were immunized intramuscularly (i.m.) plus intranasally (i.n.) with plasmid DNA containing the coding sequence of a *C. pneumoniae* polypeptide. Saline or the plasmid vector lacking an inserted chlamydial gene was given to groups of control animals.

25 For i.m. immunization, alternate left and right quadriceps were injected with 100µg of DNA in 50µl of PBS on three occasions at 0, 3 and 6 weeks. For i.n. immunization, anaesthetized mice aspirated 50µl of PBS containing 50 µg DNA on three occasions at 0, 3 and 6 weeks. At week 8, immunized mice 30 were inoculated i.n. with  $5 \times 10^5$  IFU of *C. pneumoniae*, strain AR39 in 100µl of SPG buffer to test their ability to limit the growth of a sublethal *C. pneumoniae* challenge.

Lungs were taken from mice at day 9 post-challenge and immediately homogenised in SPG buffer (7.5% sucrose, 5mM glutamate, 12.5mM phosphate pH7.5). The homogenate was stored frozen at -70°C until assay. Dilutions of the homogenate were assayed for the presence of infectious chlamydia by inoculation onto monolayers of susceptible cells. The inoculum was centrifuged onto the cells at 3000rpm for 1 hour, then the cells were incubated for three days at 35°C in the presence of 1µg/ml cycloheximide. After incubation the monolayers were fixed with 10 formalin and methanol then immunoperoxidase stained for the presence of chlamydial inclusions using convalescent sera from rabbits infected with *C. pneumoniae* and metal-enhanced DAB as a peroxidase substrate.

Consistent with the first aspect of the invention, polypeptide derivatives are provided that are partial sequences of SEQ ID Nos: 14 to 26, partial sequences of polypeptide sequences homologous to SEQ ID Nos: 14 to 26, polypeptides derived from full-length polypeptides by internal deletion, and fusion proteins.

It is an accepted practice in the field of immunology to use fragments and variants of protein immunogens as vaccines, as all that is required to induce an immune response to a protein is a small (e.g., 8 to 10 amino acid) immunogenic region of the protein. Various short synthetic peptides corresponding to surface-exposed antigens of pathogens other than *Chlamydia* have been shown to be effective vaccine antigens against their respective pathogens, e.g. an 11 residue peptide of murine mammary tumor virus (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539), a 16-residue peptide of Semliki Forest virus (Snijders et al., 1991. J. Gen. Virol. 72:557-565), and two overlapping peptides of 15 residues each from canine parvovirus (Langeveld et al., Vaccine 12(15):1473-1480, 1994).

Accordingly, it will be readily apparent to one skilled in the art, having read the present description, that partial

sequences of SEQ ID Nos: 14 to 26 or their homologous amino acid sequences are inherent to the full-length sequences and are taught by the present invention. Such polypeptide fragments preferably are at least 12 amino acids in length.

- 5 Advantageously, they are at least 20 amino acids, preferably at least 50 amino acids, more preferably at least 75 amino acids, and most preferably at least 100 amino acids in length.

Polynucleotides of 30 to 600 nucleotides encoding partial sequences of sequences homologous to SEQ ID Nos: 14 to 26 are  
10 retrieved by PCR amplification using the parameters outlined above and using primers matching the sequences upstream and downstream of the 5' and 3' ends of the fragment to be amplified. The template polynucleotide for such amplification is either the full length polynucleotide homologous to one of  
15 SEQ ID Nos: 1 to 13, or a polynucleotide contained in a mixture of polynucleotides such as a DNA or RNA library. As an alternative method for retrieving the partial sequences, screening hybridization is carried out under conditions described above and using the formula for calculating  $T_m$ . Where  
20 fragments of 30 to 600 nucleotides are to be retrieved, the calculated  $T_m$  is corrected by subtracting (600/polynucleotide size in base pairs) and the stringency conditions are defined by a hybridization temperature that is 5 to 10°C below  $T_m$ . Where oligonucleotides shorter than 20-30 bases are to be obtained,  
25 the formula for calculating the  $T_m$  is as follows:  $T_m = 4 \times (G+C) + 2 \times (A+T)$ . For example, an 18 nucleotide fragment of 50% G+C would have an approximate  $T_m$  of 54°C. Short peptides that are fragments of SEQ. ID Nos. 14 to 26 or their homologous sequences, are obtained directly by chemical synthesis (E. Gross  
30 and H. J. Meinhofer, 4 The Peptides: Analysis, Synthesis, Biology; Modern Techniques of Peptide Synthesis, John Wiley & Sons (1981), and M. Bodanzki, Principles of Peptide Synthesis, Springer -Verlag (1984)).

Useful polypeptide derivatives, e.g., polypeptide fragments, are designed using computer-assisted analysis of amino acid sequences. This identifies probable surface-exposed, antigenic regions (Hughes et al., 1992. *Infect. Immun.*

5 60(9):3497). An analysis of the 6 amino acid sequences contained in SEQ ID Nos: 14 to 26, based on the product of flexibility and hydrophobicity propensities using the program SEQSEE (Wishart DS, et al. "SEQSEE: a comprehensive program suite for protein sequence analysis." *Comput Appl Biosci.* 1994

10 Apr;10(2):121-32), reveal a number of potential B- and T-cell epitopes which may be used as a basis for selecting useful immunogenic fragments and variants. The results are shown in Figures 11 to 15. This analysis uses a reasonable combination of external surface features that is likely to be recognized by  
15 antibodies. Probable T-cell epitopes for HLA-A0201 MHC subclass were revealed by an algorithm written at Connaught Laboratories that emulates an approach developed at the NIH (Parker KC, et al. "Peptide binding to MHC class I molecules: implications for antigenic peptide prediction." *Immunol Res* 1995;14(1):34-57).

20 Epitopes which induce a protective T cell-dependent immune response are present throughout the length of the polypeptide. However, some epitopes may be masked by secondary and tertiary structures of the polypeptide. To reveal such masked epitopes large internal deletions are created which  
25 remove much of the original protein structure and expose the masked epitopes. Such internal deletions sometimes effect the additional advantage of removing immunodominant regions of high variability among strains.

Polynucleotides encoding polypeptide fragments and  
30 polypeptides having large internal deletions are constructed using standard methods (Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons Inc., 1994). Such methods include standard PCR, inverse PCR, restriction enzyme treatment of cloned DNA molecules, or the method of Kunkel et al.

(Kunkel et al. Proc. Natl. Acad. Sci. USA (1985) 82:448).

Components for these methods and instructions for their use are readily available from various commercial sources such as Stratagene. Once the deletion mutants have been constructed, they are tested for their ability to prevent or treat Chlamydia infection as described above.

As used herein, a fusion polypeptide is one that contains a polypeptide or a polypeptide derivative of the invention fused at the N- or C-terminal end to any other polypeptide

(hereinafter referred to as a peptide tail). A simple way to obtain such a fusion polypeptide is by translation of an in-frame fusion of the polynucleotide sequences, i.e., a hybrid gene. The hybrid gene encoding the fusion polypeptide is inserted into an expression vector which is used to transform or transfect a host cell. Alternatively, the polynucleotide sequence encoding the polypeptide or polypeptide derivative is inserted into an expression vector in which the polynucleotide encoding the peptide tail is already present. Such vectors and instructions for their use are commercially available, e.g. the pMal-c2 or pMal-p2 system from New England Biolabs, in which the peptide tail is a maltose binding protein, the glutathione-S-transferase system of Pharmacia, or the His-Tag system available from Novagen. These and other expression systems provide convenient means for further purification of polypeptides and derivatives of the invention.

An advantageous example of a fusion polypeptide is one where the polypeptide or homolog or fragment of the invention is fused to a polypeptide having adjuvant activity, such as subunit B of either cholera toxin or *E. coli* heat-labile toxin. Another advantageous fusion is one where the polypeptide, homolog or fragment is fused to a strong T-cell epitope or B-cell epitope. Such an epitope may be one known in the art (e.g. the Hepatitis B virus core antigen, D.R. Millich et al., "Antibody production to the nucleocapsid and envelope of the Hepatitis B virus primed

by a single synthetic T cell site", Nature. 1987. 329:547-549), or one which has been identified in another polypeptide of the invention (Figures 11-15). Consistent with this aspect of the invention is a fusion polypeptide comprising T- or B-cell  
5 epitopes from one of SEQ ID Nos: 14 to 26 or its homolog or fragment, wherein the epitopes are derived from multiple variants of said polypeptide or homolog or fragment, each variant differing from another in the location and sequence of its epitope within the polypeptide. Such a fusion is effective  
10 in the prevention and treatment of Chlamydia infection since it optimizes the T- and B-cell response to the overall polypeptide, homolog or fragment.

To effect fusion, the polypeptide of the invention is fused to the N-, or preferably, to the C-terminal end of the  
15 polypeptide having adjuvant activity or T- or B-cell epitope. Alternatively, a polypeptide fragment of the invention is inserted internally within the amino acid sequence of the polypeptide having adjuvant activity. The T- or B-cell epitope may also be inserted internally within the amino acid sequence  
20 of the polypeptide of the invention.

Consistent with the first aspect, the polynucleotides of the invention also encode hybrid precursor polypeptides containing heterologous signal peptides, which mature into polypeptides of the invention. By "heterologous signal peptide"  
25 is meant a signal peptide that is not found in naturally-occurring precursors of polypeptides of the invention.

A polynucleotide molecule according to the invention, including RNA, DNA, or modifications or combinations thereof, has various applications. A DNA molecule is used, for example,  
30 (i) in a process for producing the encoded polypeptide in a recombinant host system, (ii) in the construction of vaccine vectors such as poxviruses, which are further used in methods and compositions for preventing and/or treating Chlamydia infection, (iii) as a vaccine agent (as well as an RNA

molecule), in a naked form or formulated with a delivery vehicle and, (iv) in the construction of attenuated *Chlamydia* strains that can over-express a polynucleotide of the invention or express it in a non-toxic, mutated form.

5 Accordingly, a second aspect of the invention encompasses (i) an expression cassette containing a DNA molecule of the invention placed under the control of the elements required for expression, in particular under the control of an appropriate promoter; (ii) an expression vector containing an expression  
10 cassette of the invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a  
15 procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow expression of the DNA molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture.

20 A recombinant expression system is selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (e.g., COS1, NIH3T3, or JEG3 cells), arthropods cells (e.g., *Spodoptera frugiperda* (SF9) cells), and plant  
25 cells. A preferred expression system is a procaryotic host such as *E. coli*. Bacterial and eucaryotic cells are available from a number of different sources including commercial sources to those skilled in the art, e.g., the American Type Culture Collection (ATCC; Rockville, Maryland). Commercial sources of  
30 cells used for recombinant protein expression also provide instructions for usage of the cells.

The choice of the expression system depends on the features desired for the expressed polypeptide. For example, it



may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form.

One skilled in the art would readily understand that not all vectors and expression control sequences and hosts would be expected to express equally well the polynucleotides of this invention. With the guidelines described below, however, a selection of vectors, expression control sequences and hosts may be made without undue experimentation and without departing from the scope of this invention.

10 In selecting a vector, the host must be chosen that is compatible with the vector which is to exist and possibly replicate in it. Considerations are made with respect to the vector copy number, the ability to control the copy number, expression of other proteins such as antibiotic resistance. In  
15 selecting an expression control sequence, a number of variables are considered. Among the important variable are the relative strength of the sequence (e.g. the ability to drive expression under various conditions), the ability to control the sequence's function, compatibility between the polynucleotide to be  
20 expressed and the control sequence (e.g. secondary structures are considered to avoid hairpin structures which prevent efficient transcription). In selecting the host, unicellular hosts are selected which are compatible with the selected vector, tolerant of any possible toxic effects of the expressed  
25 product, able to secrete the expressed product efficiently if such is desired, to be able to express the product in the desired conformation, to be easily scaled up, and to which ease of purification of the final product.

The choice of the expression cassette depends on the host  
30 system selected as well as the features desired for the expressed polypeptide. Typically, an expression cassette includes a promoter that is functional in the selected host system and can be constitutive or inducible; a ribosome binding site; a start codon (ATG) if necessary; a region encoding a

signal peptide, e.g., a lipidation signal peptide; a DNA molecule of the invention; a stop codon; and optionally a 3' terminal region (translation and/or transcription terminator). The signal peptide encoding region is adjacent to the polynucleotide of the invention and placed in proper reading frame. The signal peptide-encoding region is homologous or heterologous to the DNA molecule encoding the mature polypeptide and is compatible with the secretion apparatus of the host used for expression. The open reading frame constituted by the DNA molecule of the invention, solely or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter *araB*) and is functional in Gram-negative bacteria such as *E. coli* (as described in U.S. Patent No. 5,028,530 and in Cagnon et al., (Cagnon et al., Protein Engineering (1991) 4(7):843)); the promoter of the gene of bacteriophage T7 encoding RNA polymerase, that is functional in a number of *E. coli* strains expressing T7 polymerase (described in U.S. Patent No. 4,952,496); *OspA* lipidation signal peptide; and *RlpB* lipidation signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (e.g., plasmids or viral vectors) can be chosen, for example, from those described in Pouwels et al. (Cloning Vectors: A Laboratory Manual 1985, Supp. 1987). Suitable expression vectors can be purchased from various commercial sources.

Methods for transforming/transfecting host cells with expression vectors are well-known in the art and depend on the

host system selected as described in Ausubel et al., (Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994).

Upon expression, a recombinant polypeptide of the  
5 invention (or a polypeptide derivative) is produced and remains  
in the intracellular compartment, is secreted/excreted in the  
extracellular medium or in the periplasmic space, or is embedded  
in the cellular membrane. The polypeptide is recovered in a  
substantially purified form from the cell extract or from the  
10 supernatant after centrifugation of the recombinant cell  
culture. Typically, the recombinant polypeptide is purified by  
antibody-based affinity purification or by other well-known  
methods that can be readily adapted by a person skilled in the  
art, such as fusion of the polynucleotide encoding the  
15 polypeptide or its derivative to a small affinity binding  
domain. Antibodies useful for purifying by immunoaffinity the  
polypeptides of the invention are obtained as described below.

A polynucleotide of the invention can also be useful as a  
vaccine. There are two major routes, either using a viral or  
20 bacterial host as gene delivery vehicle (live vaccine vector) or  
administering the gene in a free form, e.g., inserted into a  
plasmid. Therapeutic or prophylactic efficacy of a  
polynucleotide of the invention is evaluated as described below.

Accordingly, a third aspect of the invention provides (i)  
25 a vaccine vector such as a poxvirus, containing a DNA molecule  
of the invention, placed under the control of elements required  
for expression; (ii) a composition of matter comprising a  
vaccine vector of the invention, together with a diluent or  
carrier; specifically (iii) a pharmaceutical composition  
30 containing a therapeutically or prophylactically effective  
amount of a vaccine vector of the invention; (iv) a method for  
inducing an immune response against *Chlamydia* in a mammal (e.g.,  
a human; alternatively, the method can be used in veterinary  
applications for treating or preventing *Chlamydia* infection of

animals, e.g., cats or birds), which involves administering to the mammal an immunogenically effective amount of a vaccine vector of the invention to elicit a protective or therapeutic immune response to *Chlamydia*; and particularly, (v) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumonia*, *C. pecorum*) infection, which involves administering a prophylactic or therapeutic amount of a vaccine vector of the invention to an infected individual. Additionally, the third aspect of the invention encompasses the use of a vaccine vector of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, a vaccine vector expresses one or several polypeptides or derivatives of the invention. The vaccine vector may express additionally a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), that enhances the immune response (adjuvant effect). It is understood that each of the components to be expressed is placed under the control of elements required for expression in a mammalian cell.

Consistent with the third aspect of the invention is a composition comprising several vaccine vectors, each of them capable of expressing a polypeptide or derivative of the invention. A composition may also comprise a vaccine vector capable of expressing an additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof, optionally together with a cytokine such as IL-2 or IL-12.

Vaccination methods for treating or preventing infection in a mammal comprises use of a vaccine vector of the invention to be administered by any conventional route, particularly to a mucosal (e.g., ocular, intranasal, oral, gastric, pulmonary, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. Preferred routes depend upon the choice of the vaccine vector. Treatment may be

5 effected in a single dose or repeated at intervals. The appropriate dosage depends on various parameters understood by skilled artisans such as the vaccine vector itself, the route of administration or the condition of the mammal to be vaccinated (weight, age and the like).

Live vaccine vectors available in the art include viral vectors such as adenoviruses and poxviruses as well as bacterial vectors, e.g., *Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, Bacille bilié de Calmette-Guérin (BCG), and  
10 *Streptococcus*.

An example of an adenovirus vector, as well as a method for constructing an adenovirus vector capable of expressing a DNA molecule of the invention, are described in U.S. Patent No. 4,920,209. Poxvirus vectors include vaccinia and canary pox  
15 virus, described in U.S. Patent No. 4,722,848 and U.S. Patent No. 5,364,773, respectively. (Also see, e.g., Tartaglia et al., Virology (1992) 188:217) for a description of a vaccinia virus vector and Taylor et al, Vaccine (1995) 13:539 for a reference of a canary pox.) Poxvirus vectors capable of expressing a  
20 polynucleotide of the invention are obtained by homologous recombination as described in Kieny et al., Nature (1984) 312:163 so that the polynucleotide of the invention is inserted in the viral genome under appropriate conditions for expression in mammalian cells. Generally, the dose of vaccine viral  
25 vector, for therapeutic or prophylactic use, can be of from about  $1 \times 10^4$  to about  $1 \times 10^{11}$ , advantageously from about  $1 \times 10^7$  to about  $1 \times 10^{10}$ , preferably of from about  $1 \times 10^7$  to about  $1 \times 10^9$  plaque-forming units per kilogram. Preferably, viral vectors are administered parenterally; for example, in 3 doses, 4 weeks  
30 apart. It is preferable to avoid adding a chemical adjuvant to a composition containing a viral vector of the invention and thereby minimizing the immune response to the viral vector itself.

Non-toxicogenic *Vibrio cholerae* mutant strains that are useful as a live oral vaccine are known. Mekalanos et al., Nature (1983) 306:551 and U.S. Patent No. 4,882,278 describe strains which have a substantial amount of the coding sequence of each of the two *ctxA* alleles deleted so that no functional *cholerae* toxin is produced. WO 92/11354 describes a strain in which the *irgA* locus is inactivated by mutation; this mutation can be combined in a single strain with *ctxA* mutations. WO 94/01533 describes a deletion mutant lacking functional *ctxA* and 10 *attRS1* DNA sequences. These mutant strains are genetically engineered to express heterologous antigens, as described in WO 94/19482. An effective vaccine dose of a *Vibrio cholerae* strain capable of expressing a polypeptide or polypeptide derivative encoded by a DNA molecule of the invention contains 15 about  $1 \times 10^5$  to about  $1 \times 10^9$ , preferably about  $1 \times 10^6$  to about  $1 \times 10^8$ , viable bacteria in a volume appropriate for the selected route of administration. Preferred routes of administration include all mucosal routes; most preferably, these vectors are administered intranasally or orally.

20 Attenuated *Salmonella typhimurium* strains, genetically engineered for recombinant expression of heterologous antigens or not, and their use as oral vaccines are described in Nakayama et al. (Bio/Technology (1988) 6:693) and WO 92/11361. Preferred routes of administration include all mucosal routes; 25 most preferably, these vectors are administered intranasally or orally.

Other bacterial strains used as vaccine vectors in the context of the present invention are described for *Shigella flexneri* in High et al., EMBO (1992) 11:1991 and Sizemore et 30 al., Science (1995) 270:299; for *Streptococcus gordonii* in Medaglini et al., Proc. Natl. Acad. Sci. USA (1995) 92:6868; and for Bacille Calmette Guerin in Flynn J.L., Cell. Mol. Biol. (1994) 40 (suppl. I):31, WO 88/06626, WO 90/00594, WO 91/13157, WO 92/01796, and WO 92/21376.

In bacterial vectors, the polynucleotide of the invention is inserted into the bacterial genome or remains in a free state as part of a plasmid.

The composition comprising a vaccine bacterial vector of the present invention may further contain an adjuvant. A number of adjuvants are known to those skilled in the art. Preferred adjuvants as provided below.

Accordingly, a fourth aspect of the invention provides (i) a composition of matter comprising a polynucleotide of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal by administration of an immunogenically effective amount of a polynucleotide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polynucleotide of the invention to an infected individual. Additionally, the fourth aspect of the invention encompasses the use of a polynucleotide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection. A preferred use includes the use of a DNA molecule placed under conditions for expression in a mammalian cell, especially in a plasmid that is unable to replicate in mammalian cells and to substantially integrate in a mammalian genome.

Uses of the polynucleotides of the invention include their administration to a mammal as a vaccine, for therapeutic or prophylactic purposes. Such polynucleotides are used in the form of DNA as part of a plasmid that is unable to replicate in a mammalian cell and unable to integrate into the mammalian genome. Typically, such a DNA molecule is placed under the

control of a promoter suitable for expression in a mammalian cell. The promoter functions either ubiquitously or tissue-specifically. Examples of non-tissue specific promoters include the early Cytomegalovirus (CMV) promoter (described in U.S.

- 5 Patent No. 4,168,062) and the Rous Sarcoma Virus promoter (described in Norton & Coffin, Molec. Cell Biol. (1985) 5:281). An example of a tissue-specific promoter is the desmin promoter which drives expression in muscle cells (Li et al., Gene (1989) 78:243, Li & Paulin, J. Biol. Chem. (1991) 266:6562 and Li & Paulin, J. Biol. Chem. (1993) 268:10403). Use of promoters is well-known to those skilled in the art. Useful vectors are described in numerous publications, specifically WO 94/21797 and Hartikka et al., Human Gene Therapy (1996) 7:1205.

- Polynucleotides of the invention which are used as  
15 vaccines encode either a precursor or a mature form of the corresponding polypeptide. In the precursor form, the signal peptide is either homologous or heterologous. In the latter case, a eucaryotic leader sequence such as the leader sequence of the tissue-type plasminogen factor (tPA) is preferred.

- 20 As used herein, a composition of the invention contains one or several polynucleotides with optionally at least one additional polynucleotide encoding another *Chlamydia* antigen such as urease subunit A, B, or both, or a fragment, derivative, mutant, or analog thereof. The composition may also contain an  
25 additional polynucleotide encoding a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12) so that the immune response is enhanced. These additional polynucleotides are placed under appropriate control for expression. Advantageously, DNA molecules of the invention and/or additional  
30 DNA molecules to be included in the same composition, are present in the same plasmid.

Standard techniques of molecular biology for preparing and purifying polynucleotides are used in the preparation of polynucleotide therapeutics of the invention. For use as a



vaccine, a polynucleotide of the invention is formulated according to various methods outlined below.

One method utilizes the polynucleotide in a naked form, free of any delivery vehicles. Such a polynucleotide is simply diluted in a physiologically acceptable solution such as sterile saline or sterile buffered saline, with or without a carrier. When present, the carrier preferably is isotonic, hypotonic, or weakly hypertonic, and has a relatively low ionic strength, such as provided by a sucrose solution, e.g., a solution containing 10 20% sucrose.

An alternative method utilizes the polynucleotide in association with agents that assist in cellular uptake. Examples of such agents are (i) chemicals that modify cellular permeability, such as bupivacaine (see, e.g., WO 94/16737), (ii) 15 liposomes for encapsulation of the polynucleotide, or (iii) cationic lipids or silica, gold, or tungsten microparticles which associate themselves with the polynucleotides.

Anionic and neutral liposomes are well-known in the art 20 (see, e.g., Liposomes: A Practical Approach, RPC New Ed, IRL press (1990), for a detailed description of methods for making liposomes) and are useful for delivering a large range of products, including polynucleotides.

Cationic lipids are also known in the art and are 25 commonly used for gene delivery. Such lipids include Lipofectin™ also known as DOTMA (N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammonium chloride), DOTAP (1,2-bis(oleyloxy)-3-(trimethylammonio)propane), DDAB (dimethyldioctadecylammonium bromide), DOGS (dioctadecylamidodloglycyl spermine) and 30 cholesterol derivatives such as DC-Chol (3 beta-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol). A description of these cationic lipids can be found in EP 187,702, WO 90/11092, U.S. Patent No. 5,283,185, WO 91/15501, WO 95/26356, and U.S. Patent No. 5,527,928. Cationic lipids for

gene delivery are preferably used in association with a neutral lipid such as DOPE (dioleoyl phosphatidylethanolamine), as described in WO 90/11092 as an example.

Formulation containing cationic liposomes may optionally contain other transfection-facilitating compounds. A number of them are described in WO 93/18759, WO 93/19768, WO 94/25608, and WO 95/02397. They include spermine derivatives useful for facilitating the transport of DNA through the nuclear membrane (see, for example, WO 93/18759) and membrane-permeabilizing compounds such as GALA, Gramicidine S, and cationic bile salts (see, for example, WO 93/19768).

Gold or tungsten microparticles are used for gene delivery, as described in WO 91/00359, WO 93/17706, and Tang et al. Nature (1992) 356:152. The microparticle-coated polynucleotide is injected via intradermal or intraepidermal routes using a needleless injection device ("gene gun"), such as those described in U.S. Patent No. 4,945,050, U.S. Patent No. 5,015,580, and WO 94/24263.

The amount of DNA to be used in a vaccine recipient depends, e.g., on the strength of the promoter used in the DNA construct, the immunogenicity of the expressed gene product, the condition of the mammal intended for administration (e.g., the weight, age, and general health of the mammal), the mode of administration, and the type of formulation. In general, a therapeutically or prophylactically effective dose from about 1  $\mu\text{g}$  to about 1 mg, preferably, from about 10  $\mu\text{g}$  to about 800  $\mu\text{g}$  and, more preferably, from about 25  $\mu\text{g}$  to about 250  $\mu\text{g}$ , can be administered to human adults. The administration can be achieved in a single dose or repeated at intervals.

The route of administration is any conventional route used in the vaccine field. As general guidance, a polynucleotide of the invention is administered via a mucosal surface, e.g., an ocular, intranasal, pulmonary, oral, intestinal, rectal, vaginal, and urinary tract surface; or via a

parenteral route, e.g., by an intravenous, subcutaneous, intraperitoneal, intradermal, intraepidermal, or intramuscular route. The choice of administration route depends on the formulation that is selected. A polynucleotide formulated in association with bupivacaine is advantageously administered into muscles. When a neutral or anionic liposome or a cationic lipid, such as DOTMA or DC-Chol, is used, the formulation can be advantageously injected via intravenous, intranasal (aerosolization), intramuscular, intradermal, and subcutaneous routes. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal, or subcutaneous routes.

Although not absolutely required, such a composition can also contain an adjuvant. If so, a systemic adjuvant that does not require concomitant administration in order to exhibit an adjuvant effect is preferable such as, e.g., QS21, which is described in U.S. Patent No. 5,057,546.

The sequence information provided in the present application enables the design of specific nucleotide probes and primers that are used for diagnostic purposes. Accordingly, a fifth aspect of the invention provides a nucleotide probe or primer having a sequence found in or derived by degeneracy of the genetic code from a sequence shown in any one of SEQ ID Nos: 1 to 13.

The term "probe" as used in the present application refers to DNA (preferably single stranded) or RNA molecules (or modifications or combinations thereof) that hybridize under the stringent conditions, as defined above, to nucleic acid molecules having SEQ ID Nos: 1 to 13 or to sequences homologous to SEQ ID Nos: 1 to 13, or to their complementary or anti-sense sequences. Generally, probes are significantly shorter than full-length sequences. Such probes contain from about 5 to about 100, preferably from about 10 to about 80, nucleotides. In particular, probes have sequences that are at least 75%,

preferably at least 85%, more preferably 95% homologous to a portion of any of SEQ ID Nos: 1 to 13 or that are complementary to such sequences. Probes may contain modified bases such as inosine, methyl-5-deoxycytidine, deoxyuridine, dimethylamino-5-deoxyuridine, or diamino-2, 6-purine. Sugar or phosphate residues may also be modified or substituted. For example, a deoxyribose residue may be replaced by a polyamide (Nielsen et al., Science (1991) 254:1497) and phosphate residues may be replaced by ester groups such as diphosphate, alkyl, arylphosphonate and phosphorothioate esters. In addition, the 2'-hydroxyl group on ribonucleotides may be modified by including such groups as alkyl groups.

Probes of the invention are used in diagnostic tests, as capture or detection probes. Such capture probes are conventionally immobilized on a solid support, directly or indirectly, by covalent means or by passive adsorption. A detection probe is labelled by a detection marker selected from: radioactive isotopes, enzymes such as peroxidase, alkaline phosphatase, and enzymes able to hydrolyze a chromogenic, fluorogenic, or luminescent substrate, compounds that are chromogenic, fluorogenic, or luminescent, nucleotide base analogs, and biotin.

Probes of the invention are used in any conventional hybridization technique, such as dot blot (Maniatis et al., Molecular Cloning: A Laboratory Manual (1982) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), Southern blot (Southern, J. Mol. Biol. (1975) 98:503), northern blot (identical to Southern blot with the exception that RNA is used as a target), or the sandwich technique (Dunn et al., Cell (1977) 12:23). The latter technique involves the use of a specific capture probe and/or a specific detection probe with nucleotide sequences that at least partially differ from each other.

A primer is a probe of usually about 10 to about 40 nucleotides that is used to initiate enzymatic polymerization of DNA in an amplification process (e.g., PCR), in an elongation process, or in a reverse transcription method. Primers used in 5 diagnostic methods involving PCR are labeled by methods known in the art.

As described herein, the invention also encompasses (i) a reagent comprising a probe of the invention for detecting and/or identifying the presence of *Chlamydia* in a biological material; 10 (ii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA or RNA is extracted from the material and denatured, and (c) exposed to a probe of the invention, for example, a capture, 15 detection probe or both, under stringent hybridization conditions, such that hybridization is detected; and (iii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA is 20 extracted therefrom, (c) the extracted DNA is primed with at least one, and preferably two, primers of the invention and amplified by polymerase chain reaction, and (d) the amplified DNA fragment is produced.

It is apparent that disclosure of polynucleotide 25 sequences of SEQ ID Nos: 1 to 13, their homolog, and partial sequences of either enable their corresponding amino acid sequences. Accordingly, a sixth aspect of the invention features a substantially purified polypeptide or polypeptide derivative having an amino acid sequence encoded by a 30 polynucleotide of the invention.

A "substantially purified polypeptide" as used herein is defined as a polypeptide that is separated from the environment in which it naturally occurs and/or that is free of the majority of the polypeptides that are present in the environment in which

it was synthesized. For example, a substantially purified polypeptide is free from cytoplasmic polypeptides. Those skilled in the art would readily understand that the polypeptides of the invention may be purified from a natural source, i.e., a *Chlamydia* strain, or produced by recombinant means.

Consistent with the sixth aspect of the invention are polypeptides, homologs or fragments which are modified or treated to enhance their immunogenicity in the target animal, in whom the polypeptide, homolog or fragments are intended to confer protection against *Chlamydia*. Such modifications or treatments include: amino acid substitutions with an amino acid derivative such as 3-methylhistidine, 4-hydroxyproline, 5-hydroxylysine etc., modifications or deletions which are carried out after preparation of the polypeptide, homolog or fragment, such as the modification of free amino, carboxyl or hydroxyl side groups of the amino acids.

Identification of homologous polypeptides or polypeptide derivatives encoded by polynucleotides of the invention which have specific antigenicity is achieved by screening for cross-reactivity with an antiserum raised against the polypeptide of reference having an amino acid sequence of any one of SEQ ID Nos: 14 to 26. The procedure is as follows: a monospecific hyperimmune antiserum is raised against a purified reference polypeptide, a fusion polypeptide (for example, an expression product of MBP, GST, or His-tag systems), or a synthetic peptide predicted to be antigenic. Where an antiserum is raised against a fusion polypeptide, two different fusion systems are employed. Specific antigenicity can be determined according to a number of methods, including Western blot (Towbin et al., Proc. Natl. Acad. Sci. USA (1979) 76:4350), dot blot, and ELISA, as described below.

In a Western blot assay, the product to be screened, either as a purified preparation or a total *E. coli* extract, is

submitted to SDS-Page electrophoresis as described by Laemmli (Nature (1970) 227:680). After transfer to a nitrocellulose membrane, the material is further incubated with the monospecific hyperimmune antiserum diluted in the range of 5 dilutions from about 1:5 to about 1:5000, preferably from about 1:100 to about 1:500. Specific antigenicity is shown once a band corresponding to the product exhibits reactivity at any of the dilutions in the above range.

In an ELISA assay, the product to be screened is 10 preferably used as the coating antigen. A purified preparation is preferred, although a whole cell extract can also be used. Briefly, about 100  $\mu$ l of a preparation at about 10  $\mu$ g protein/ml are distributed into wells of a 96-well polycarbonate ELISA plate. The plate is incubated for 2 hours at 37°C then 15 overnight at 4°C. The plate is washed with phosphate buffer saline (PBS) containing 0.05% Tween 20 (PBS/Tween buffer). The wells are saturated with 250  $\mu$ l PBS containing 1% bovine serum albumin (BSA) to prevent non-specific antibody binding. After a 1 hour incubation at 37°C, the plate is washed with PBS/Tween 20 buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100  $\mu$ l of dilutions are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when 25 specific antibodies were raised in rabbits. Incubation is carried out for 90 minutes at 37°C and the plate is washed. The reaction is developed with the appropriate substrate and the reaction is measured by colorimetry (absorbance measured spectrophotometrically). Under the above experimental 30 conditions, a positive reaction is shown by O.D. values greater than a non-immune control serum.

In a dot blot assay, a purified product is preferred, although a whole cell extract can also be used. Briefly, a solution of the product at about 100  $\mu$ g/ml is serially two-fold

diluted in 50 mM Tris-HCl (pH 7.5). 100  $\mu$ l of each dilution are applied to a nitrocellulose membrane 0.45  $\mu$ m set in a 96-well dot blot apparatus (Biorad). The buffer is removed by applying vacuum to the system. Wells are washed by addition of 50 mM

5 Tris-HCl (pH 7.5) and the membrane is air-dried. The membrane is saturated in blocking buffer (50 mM Tris-HCl (pH 7.5) 0.15 M NaCl, 10 g/L skim milk) and incubated with an antiserum dilution from about 1:50 to about 1:5000, preferably about 1:500. The reaction is revealed according to standard procedures. For

10 example, a goat anti-rabbit peroxidase conjugate is added to the wells when rabbit antibodies are used. Incubation is carried out 90 minutes at 37°C and the blot is washed. The reaction is developed with the appropriate substrate and stopped. The reaction is measured visually by the appearance of a colored  
15 spot, e.g., by colorimetry. Under the above experimental conditions, a positive reaction is shown once a colored spot is associated with a dilution of at least about 1:5, preferably of at least about 1:500.

Therapeutic or prophylactic efficacy of a polypeptide or  
20 derivative of the invention can be evaluated as described below.

A seventh aspect of the invention provides (i) a composition of matter comprising a polypeptide of the invention together with a diluent or carrier; specifically (ii) a pharmaceutical composition containing a therapeutically or prophylactically

25 effective amount of a polypeptide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal, by administering to the mammal an immunogenically effective amount of a polypeptide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv)

30 a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polypeptide of the invention to an infected individual. Additionally, the seventh aspect of the invention encompasses



the use of a polypeptide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, the immunogenic compositions of the invention are administered by conventional routes known the vaccine field, in particular to a mucosal (e.g., ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. The choice of administration route depends upon a number of parameters, such as the adjuvant associated with the polypeptide. If a mucosal adjuvant is used, the intranasal or oral route is preferred. If a lipid formulation or an aluminum compound is used, the parenteral route is preferred with the sub-cutaneous or intramuscular route being most preferred. The choice also depends upon the nature of the vaccine agent. For example, a polypeptide of the invention fused to CTB or LTB is best administered to a mucosal surface.

As used herein, the composition of the invention contains one or several polypeptides or derivatives of the invention. The composition optionally contains at least one additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof.

For use in a composition of the invention, a polypeptide or derivative thereof is formulated into or with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS, or virus-like-particles (VLPs) to facilitate delivery and/or enhance the immune response. These compounds are readily available to one skilled in the art; for example, see Liposomes: A Practical Approach, RPC New Ed, IRL press (1990).

Adjuvants other than liposomes and the like are also used and are known in the art. Adjuvants may protect the antigen from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete

factors that are chemotactic for macrophages and other components of the immune system. An appropriate selection can conventionally be made by those skilled in the art, for example, from those described below (see the eleventh aspect of the invention).

Treatment is achieved in a single dose or repeated as necessary at intervals, as can be determined readily by one skilled in the art. For example, a priming dose is followed by three booster doses at weekly or monthly intervals. An appropriate dose depends on various parameters including the recipient (e.g., adult or infant), the particular vaccine antigen, the route and frequency of administration, the presence/absence or type of adjuvant, and the desired effect (e.g., protection and/or treatment), as can be determined by one skilled in the art. In general, a vaccine antigen of the invention is administered by a mucosal route in an amount from about 10  $\mu$ g to about 500 mg, preferably from about 1 mg to about 200 mg. For the parenteral route of administration, the dose usually does not exceed about 1 mg, preferably about 100  $\mu$ g.

When used as vaccine agents, polynucleotides and polypeptides of the invention may be used sequentially as part of a multistep immunization process. For example, a mammal is initially primed with a vaccine vector of the invention such as a pox virus, e.g., via the parenteral route, and then boosted twice with the polypeptide encoded by the vaccine vector, e.g., via the mucosal route. In another example, liposomes associated with a polypeptide or derivative of the invention is also used for priming, with boosting being carried out mucosally using a soluble polypeptide or derivative of the invention in combination with a mucosal adjuvant (e.g., LT).

A polypeptide derivative of the invention is also used in accordance with the seventh aspect as a diagnostic reagent for detecting the presence of anti-*Chlamydia* antibodies, e.g., in a blood sample. Such polypeptides are about 5 to about 80,

preferably about 10 to about 50 amino acids in length. They are either labeled or unlabeled, depending upon the diagnostic method. Diagnostic methods involving such a reagent are described below.

5       Upon expression of a DNA molecule of the invention, a polypeptide or polypeptide derivative is produced and purified using known laboratory techniques. As described above, the polypeptide or polypeptide derivative may be produced as a fusion protein containing a fused tail that facilitates  
10 purification. The fusion product is used to immunize a small mammal, e.g., a mouse or a rabbit, in order to raise antibodies against the polypeptide or polypeptide derivative (monospecific antibodies). Accordingly, an eighth aspect of the invention provides a monospecific antibody that binds to a polypeptide or  
15 polypeptide derivative of the invention.

By "monospecific antibody" is meant an antibody that is capable of reacting with a unique naturally-occurring *Chlamydia* polypeptide. An antibody of the invention is either polyclonal or monoclonal. Monospecific antibodies may be recombinant,  
20 e.g., chimeric (e.g., constituted by a variable region of murine origin associated with a human constant region), humanized (a human immunoglobulin constant backbone together with hypervariable region of animal, e.g., murine, origin), and/or single chain. Both polyclonal and monospecific antibodies may  
25 also be in the form of immunoglobulin fragments, e.g., F(ab)'2 or Fab fragments. The antibodies of the invention are of any isotype, e.g., IgG or IgA, and polyclonal antibodies are of a single isotype or a mixture of isotypes.

Antibodies against the polypeptides, homologs or  
30 fragments of the present invention are generated by immunization of a mammal with a composition comprising said polypeptide, homolog or fragment. Such antibodies may be polyclonal or monoclonal. Methods to produce polyclonal or monoclonal antibodies are well known in the art. For a review, see

"Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Eds. E. Harlow and D. Lane (1988), and D.E. Yelton et al., 1981. Ann. Rev. Biochem. 50:657-680. For monoclonal antibodies, see Kohler and Milstein (1975) Nature. 256:495-497.

5       The antibodies of the invention, which are raised to a polypeptide or polypeptide derivative of the invention, are produced and identified using standard immunological assays, e.g., Western blot analysis, dot blot assay, or ELISA (see, e.g., Coligan et al., Current Protocols in Immunology (1994) 10 John Wiley & Sons, Inc., New York, NY). The antibodies are used in diagnostic methods to detect the presence of a *Chlamydia* antigen in a sample, such as a biological sample. The antibodies are also used in affinity chromatography for purifying a polypeptide or polypeptide derivative of the 15 invention. As is discussed further below, such antibodies may be used in prophylactic and therapeutic passive immunization methods.

Accordingly, a ninth aspect of the invention provides (i) a reagent for detecting the presence of *Chlamydia* in a 20 biological sample that contains an antibody, polypeptide, or polypeptide derivative of the invention; and (ii) a diagnostic method for detecting the presence of *Chlamydia* in a biological sample, by contacting the biological sample with an antibody, a polypeptide, or a polypeptide derivative of the invention, such 25 that an immune complex is formed, and by detecting such complex to indicate the presence of *Chlamydia* in the sample or the organism from which the sample is derived.

Those skilled in the art will readily understand that the immune complex is formed between a component of the sample and 30 the antibody, polypeptide, or polypeptide derivative, whichever is used, and that any unbound material is removed prior to detecting the complex. It is understood that a polypeptide reagent is useful for detecting the presence of anti-*Chlamydia* antibodies in a sample, e.g., a blood sample, while an antibody

of the invention is used for screening a sample, such as a gastric extract or biopsy, for the presence of *Chlamydia* polypeptides.

For diagnostic applications, the reagent (i.e., the antibody, polypeptide, or polypeptide derivative of the invention) is either in a free state or immobilized on a solid support, such as a tube, a bead, or any other conventional support used in the field. Immobilization is achieved using direct or indirect means. Direct means include passive adsorption (non-covalent binding) or covalent binding between the support and the reagent. By "indirect means" is meant that an anti-reagent compound that interacts with a reagent is first attached to the solid support. For example, if a polypeptide reagent is used, an antibody that binds to it can serve as an anti-reagent, provided that it binds to an epitope that is not involved in the recognition of antibodies in biological samples. Indirect means may also employ a ligand-receptor system, for example, where a molecule such as a vitamin is grafted onto the polypeptide reagent and the corresponding receptor immobilized on the solid phase. This is illustrated by the biotin-streptavidin system. Alternatively, a peptide tail is added chemically or by genetic engineering to the reagent and the grafted or fused product immobilized by passive adsorption or covalent linkage of the peptide tail.

Such diagnostic agents may be included in a kit which also comprises instructions for use. The reagent is labeled with a detection means which allows for the detection of the reagent when it is bound to its target. The detection means may be a fluorescent agent such as fluorescein isocyanate or fluorescein isothiocyanate, or an enzyme such as horse radish peroxidase or luciferase or alkaline phosphatase, or a radioactive element such as  $^{125}\text{I}$  or  $^{51}\text{Cr}$ .

Accordingly, a tenth aspect of the invention provides a process for purifying, from a biological sample, a polypeptide

or polypeptide derivative of the invention, which involves carrying out antibody-based affinity chromatography with the biological sample, wherein the antibody is a monospecific antibody of the invention.

For use in a purification process of the invention, the antibody is either polyclonal or monospecific, and preferably is of the IgG type. Purified IgGs is prepared from an antiserum using standard methods (see, e.g., Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). Conventional chromatography supports, as well as standard methods for grafting antibodies, are described in, e.g., Antibodies: A Laboratory Manual, D. Lane, E. Harlow, Eds. (1988) and outlined below.

Briefly, a biological sample, such as a *C. pneumoniae* extract preferably in a buffer solution, is applied to a chromatography material, preferably equilibrated with the buffer used to dilute the biological sample so that the polypeptide or polypeptide derivative of the invention (i.e., the antigen) is allowed to adsorb onto the material. The chromatography material, such as a gel or a resin coupled to an antibody of the invention, is in either a batch form or a column. The unbound components are washed off and the antigen is then eluted with an appropriate elution buffer, such as a glycine buffer or a buffer containing a chaotropic agent, e.g., guanidine HCl, or high salt concentration (e.g., 3 M MgCl<sub>2</sub>). Eluted fractions are recovered and the presence of the antigen is detected, e.g., by measuring the absorbance at 280 nm.

An eleventh aspect of the invention provides (i) a composition of matter comprising a monospecific antibody of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a monospecific antibody of the invention, and (iii) a method for treating or preventing a Chlamydia (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae* or

*C. pecorum*) infection, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an infected individual. Additionally, the eleventh aspect of the invention encompasses the use of a monospecific antibody of the invention in the preparation of a medicament for treating or preventing *Chlamydia* infection.

The monospecific antibody is either polyclonal or monoclonal, preferably of the IgA isotype (predominantly). In passive immunization, the antibody is administered to a mucosal surface of a mammal, e.g., the gastric mucosa, e.g., orally or intragastrically, advantageously, in the presence of a bicarbonate buffer. Alternatively, systemic administration, not requiring a bicarbonate buffer, is carried out. A monospecific antibody of the invention is administered as a single active component or as a mixture with at least one monospecific antibody specific for a different *Chlamydia* polypeptide. The amount of antibody and the particular regimen used are readily determined by one skilled in the art. For example, daily administration of about 100 to 1,000 mg of antibodies over one week, or three doses per day of about 100 to 1,000 mg of antibodies over two or three days, are effective regimens for most purposes.

Therapeutic or prophylactic efficacy are evaluated using standard methods in the art, e.g., by measuring induction of a mucosal immune response or induction of protective and/or therapeutic immunity, using, e.g., the *C. pneumoniae* mouse model. Those skilled in the art will readily recognize that the *C. pneumoniae* strain of the model may be replaced with another *Chlamydia* strain. For example, the efficacy of DNA molecules and polypeptides from *C. pneumoniae* is preferably evaluated in a mouse model using *C. pneumoniae* strain. Protection is determined by comparing the degree of *Chlamydia* infection to that of a control group. Protection is shown when infection is reduced by comparison to the control group. Such an evaluation

is made for polynucleotides, vaccine vectors, polypeptides and derivatives thereof, as well as antibodies of the invention.

Adjuvants useful in any of the vaccine compositions described above are as follows.

5 Adjuvants for parenteral administration include aluminum compounds, such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen is precipitated with, or adsorbed onto, the aluminum compound according to standard protocols. Other adjuvants, such as RIBI (ImmunoChem, Hamilton,  
10 MT), are used in parenteral administration.

Adjuvants for mucosal administration include bacterial toxins, e.g., the cholera toxin (CT), the *E. coli* heat-labile toxin (LT), the *Clostridium difficile* toxin A and the pertussis toxin (PT), or combinations, subunits, toxoids, or mutants  
15 thereof such as a purified preparation of native cholera toxin subunit B (CTB). Fragments, homologs, derivatives, and fusions to any of these toxins are also suitable, provided that they retain adjuvant activity. Preferably, a mutant having reduced toxicity is used. Suitable mutants are described, e.g., in  
20 WO 95/17211 (Arg-7-Lys CT mutant), WO 96/06627 (Arg-192-Gly LT mutant), and WO 95/34323 (Arg-9-Lys and Glu-129-Gly PT mutant). Additional LT mutants that are used in the methods and compositions of the invention include, e.g., Ser-63-Lys, Ala-69-Gly, Glu-110-Asp, and Glu-112-Asp mutants. Other adjuvants,  
25 such as a bacterial monophosphoryl lipid A (MPLA) of, e.g., *E. coli*, *Salmonella minnesota*, *Salmonella typhimurium*, or *Shigella flexneri*; saponins, or polylactide glycolide (PLGA) microspheres, are also be used in mucosal administration.

Adjuvants useful for both mucosal and parenteral  
30 administrations include polyphosphazene (WO 95/02415), DC-chol (3 b-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol; U.S. Patent No. 5,283,185 and WO 96/14831) and QS-21 (WO 88/09336).



Any pharmaceutical composition of the invention containing a polynucleotide, a polypeptide, a polypeptide derivative, or an antibody of the invention, is manufactured in a conventional manner. In particular, it is formulated with a pharmaceutically acceptable diluent or carrier, e.g., water or a saline solution such as phosphate buffer saline. In general, a diluent or carrier is selected on the basis of the mode and route of administration, and standard pharmaceutical practice. Suitable pharmaceutical carriers or diluents, as well as pharmaceutical necessities for their use in pharmaceutical formulations, are described in *Remington's Pharmaceutical Sciences*, a standard reference text in this field and in the USP/NF.

The invention also includes methods in which *Chlamydia* infection are treated by oral administration of a *Chlamydia* polypeptide of the invention and a mucosal adjuvant, in combination with an antibiotic, an antacid, sucralfate, or a combination thereof. Examples of such compounds that can be administered with the vaccine antigen and the adjuvant are antibiotics, including, e.g., macrolides, tetracyclines, and derivatives thereof (specific examples of antibiotics that can be used include azithromycin or doxycycline or immunomodulators such as cytokines or steroids). In addition, compounds containing more than one of the above-listed components coupled together, are used. The invention also includes compositions for carrying out these methods, i.e., compositions containing a *Chlamydia* antigen (or antigens) of the invention, an adjuvant, and one or more of the above-listed compounds, in a pharmaceutically acceptable carrier or diluent.

Amounts of the above-listed compounds used in the methods and compositions of the invention are readily determined by one skilled in the art. Treatment/immunization schedules are also known and readily designed by one skilled in the art. For example, the non-vaccine components can be administered on days



CLAIMS:

1. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any of:
- 5 (a) SEQ ID Nos: 15 to 26;
- (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified
- 10 polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).
2. A nucleic acid molecule comprising a nucleic acid sequence selected from any of:
- 15 (a) SEQ ID Nos: 2 to 13;
- (b) a sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 2 to 13;
- (c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a)
- 20 and (b); and
- (d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to any one of the polypeptides encoded by SEQ ID Nos: 2 to 13.
- 25 3. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 1 or 2.
4. A nucleic acid molecule comprising a nucleic acid
- 30 sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and a second polypeptide.
5. The nucleic acid molecule of claim 4 wherein the
- 35 second polypeptide is a heterologous signal peptide.

6. The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.

7. A nucleic acid molecule according to any one of claims 1 to 6, operatively linked to one or more expression control sequences.

8. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

- 10 (i) SEQ ID Nos: 1 to 13;
- (ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
- (iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid
- 15 sequences of (i) and (ii);
- (iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;
- (v) a nucleic acid sequence which encodes a polypeptide
- 20 whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;
- (vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and
- (vii) a nucleic acid sequence which encodes a polypeptide
- 25 as defined in (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (v) or the corresponding fragment of (vi);
- 30 wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

9. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

5 (i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

10 (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

15 (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

25 wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the first polypeptide.

30

10. The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

11. The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

35

12. The vaccine of any one of claims 8 to 11 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

5 13. A vaccine comprising at least one first nucleic acid according to any one of claims 1, 2, and 4 to 7 and a vaccine vector wherein each first nucleic acid is expressed as a polypeptide, the vaccine optionally comprising a second nucleic acid encoding an additional polypeptide which enhances the  
10 immune response to the polypeptide expressed by said first nucleic acid.

14. The vaccine of any one of claims 8 to 13 wherein the second nucleic acid encodes an additional *Chlamydia*  
15 polypeptide.

15. A pharmaceutical composition comprising a nucleic acid according to any one of claims 1 to 7 and a pharmaceutically acceptable carrier.

20 16. A pharmaceutical composition comprising a vaccine according to any one of claims 8 to 14 and a pharmaceutically acceptable carrier.

25 17. A unicellular host transformed with the nucleic acid molecule of claim 7.

18. An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any  
30 one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. An isolated primer of 10 to 40 nucleotides which  
35 hybridizes under stringent conditions to any one of nucleic

acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

20. A polypeptide encoded by a nucleic acid sequence  
5 according to any one of claims 1, 2 and 4 to 7.

21. A polypeptide comprising an amino acid sequence selected from any of:

- (a) SEQ ID Nos: 15 to 26;
- 10 (b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and
- (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to
- 15 the corresponding polypeptide of (a) or (b).

22. A fusion protein comprising a polypeptide of claim 20 or 21 and a second polypeptide.

20 23. The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

25

25. A method for producing a polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24, comprising the step of culturing a unicellular host of claim 17.

30

26. An antibody against the polypeptide of claim 20 or 21, or against a fusion protein of any one of claims 22 to 24.

27. A vaccine comprising at least one first polypeptide selected from any of:

35 (i) a polypeptide encoded by any one of

SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

5 (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

10 (v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (iv) or an immunogenic fragment as defined in (v) which has been modified without loss  
15 of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v);

wherein the vaccine optionally comprises an  
20 additional polypeptide which enhances the immune response to the first polypeptide.

28. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

25 (a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of  
SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of  
30 SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of  
SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one  
35 of SEQ ID Nos: 14 to 26;



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(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

10 (b) a second polypeptide;

wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

29. The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

31. A vaccine comprising at least one first polypeptide according to any one of claims 20 to 24, optionally comprising an additional polypeptide which enhances the immune response to the first polypeptide.

32. The vaccine of any one of claims 27 to 31 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

33. A pharmaceutical composition comprising a polypeptide according to any one of claims 20 to 24 and a pharmaceutically acceptable carrier.

34. A pharmaceutical composition comprising a vaccine according to any one of claims 27 to 32 and a pharmaceutically acceptable carrier.

35. A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

5

36. A method for preventing or treating *Chlamydia* infection using:

- (a) the nucleic acid of any one of claims 1 to 7;
- (b) the vaccine of any one of claims 8 to 14 and 27 to

10 32;

(c) the pharmaceutical composition of any one of claims 15, 16 and 33 to 35;

(d) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; or

15 (e) the antibody of claim 26.

37. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of;

- 20 (a) the nucleic acid of any one of claims 1 to 7;
- (b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and
- (c) the antibody of claim 26.

25 38. A diagnostic kit comprising instructions for use and a component selected from any one of:

- (a) the nucleic acid of any one of claims 1 to 7;
- (b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and

30 (c) the antibody of claim 26.

39. A method for identifying a polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24 which induces an immune response effective to prevent or lessen the

severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide or fusion protein; and

- 5 (b) inoculating the immunized mouse with *Chlamydia*, wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

- 10 40. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any of:

(a) SEQ ID No: 14;

(b) an immunogenic fragment comprising at least 50 consecutive amino acids from a polypeptide of (a); and

- 15 (c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

- 20 41. A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID No: 1;

(b) a sequence which encodes a polypeptide encoded by SEQ ID No: 1;

- 25 (c) a sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;

(d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1; and

- 30 (e) a sequence comprising at least 100 consecutive nucleotides from a nucleic acid sequence of (b).

42. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of  
35 claim 40.

43. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 40 and a second polypeptide.

5

44. The nucleic acid molecule of claim 43 wherein the second polypeptide is a heterologous signal peptide.

45. The nucleic acid molecule of claim 43 wherein the  
10 second polypeptide has adjuvant activity.

46. A nucleic acid molecule according to any one of claims 40 to 45, operatively linked to one or more expression control sequences.

15

47. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID No: 1;

(ii) a nucleic acid sequence which encodes a polypeptide  
20 encoded by SEQ ID No: 1;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide  
25 which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;

(v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 14;

(vi) a nucleic acid sequence which encodes an immunogenic  
30 fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vii) a nucleic acid sequence which encodes a polypeptide as defined in (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein  
35 said modified polypeptide or fragment is at least 75% identical

in amino acid sequence to the corresponding polypeptide of (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second  
5 nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

48. A vaccine comprising a vaccine vector and at least  
10 one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by SEQ ID No: 1;

(ii) a polypeptide encoded by a nucleic acid sequence  
15 comprising at least 38 consecutive nucleotides from  
SEQ ID No: 1;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;

(iv) a polypeptide whose sequence is set forth in  
20 SEQ ID No: 14;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss  
25 of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

30 wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the first polypeptide.

35

49. The vaccine of claim 48 wherein the second polypeptide is a heterologous signal peptide.

50. The vaccine of claim 48 wherein the second  
5 polypeptide has adjuvant activity.

51. The vaccine of any one of claims 47 to 50 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

10

52. A vaccine comprising at least one first nucleic acid according to any one of claims 40, 41, and 43 to 46 and a vaccine vector wherein each first nucleic acid is expressed as a polypeptide, the vaccine optionally comprising a second  
15 nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by said first nucleic acid.

20

53. The vaccine of any one of claims 47 to 52 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

25

54. A pharmaceutical composition comprising a nucleic acid according to any one of claims 40 to 46 and a pharmaceutically acceptable carrier.

30

55. A pharmaceutical composition comprising a vaccine according to any one of claims 47 to 53 and a pharmaceutically acceptable carrier.

56. A unicellular host transformed with the nucleic acid molecule of claim 46.

35

57. An isolated nucleic acid probe of 5 to 100 nucleotides which are at least 75% similar to the nucleic acid

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molecule of SEQ ID No: 1, or to a complementary or anti-sense sequence of said nucleic acid molecule.

58. An isolated primer of 10 to 40 nucleotides which  
5 which are at least 75% similar to the nucleic acid molecules of  
SEQ ID No: 1, or to a complementary or anti-sense sequence of  
said nucleic acid molecule.

59. A polypeptide encoded by a nucleic acid sequence  
10 according to any one of claims 40, 41 and 43 to 46.

60. A polypeptide comprising an amino acid sequence  
selected from any of;

(d) SEQ ID No: 14;

15 (e) an immunogenic fragment comprising at least 12  
consecutive amino acids from a polypeptide of (a); and

(f) a polypeptide of (a) or (b) which has been modified  
without loss of immunogenicity, wherein said modified  
polypeptide is at least 75% identical in amino acid sequence to  
20 the corresponding polypeptide of (a) or (b).

61. A fusion protein comprising a polypeptide of claim 59  
or 60 and a second polypeptide.

25 62. The fusion protein of claim 61 wherein the second  
polypeptide is a heterologous signal peptide.

63. The fusion protein of claim 61 wherein the second  
polypeptide has adjuvant activity.

30

64. A method for producing a polypeptide of claim 59 or  
60, or a fusion protein of any one of claims 61 to 63,  
comprising the step of culturing a unicellular host of claim  
56.

65. An antibody against the polypeptide of claim 59 or 60, or against a fusion protein of any one of claims 61 to 63.

66. A vaccine comprising at least one first polypeptide selected from any of:

- (i) a polypeptide encoded by SEQ ID No: 1;
- (ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;
- (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;
- (iv) a polypeptide whose sequence is set forth in SEQ ID No: 14;

- (v) an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 14; and
- (vi) a polypeptide as defined in (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v);

wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

67. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

- (a) a first polypeptide selected from any of:
  - (i) a polypeptide encoded by SEQ ID No: 1;
  - (ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;
  - (iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;
  - (iii) a polypeptide whose sequence is set forth in



SEQ ID No: 14;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide; wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

68. The vaccine of claim 67 wherein the second polypeptide is a heterologous signal peptide.

69. The vaccine of claim 67 wherein the second polypeptide has adjuvant activity.

70. A vaccine comprising at least one first polypeptide according to any one of claims 59 to 63, optionally comprising an additional polypeptide which enhances the immune response to the first polypeptide.

71. The vaccine of any one of claims 66 to 70 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

72. A pharmaceutical composition comprising a polypeptide according to any one of claims 59 to 63 and a pharmaceutically acceptable carrier.

73. A pharmaceutical composition comprising a vaccine according to any one of claims 66 to 71 and a pharmaceutically acceptable carrier.

74. A pharmaceutical composition comprising an antibody according to claim 65 and a pharmaceutically acceptable carrier.

5 75. A method for preventing or treating *Chlamydia* infection using:

(f) the nucleic acid of any one of claims 40 to 46;

(g) the vaccine of any one of claims 47 to 53 and 66 to 71;

10 (h) the pharmaceutical composition of any one of claims 54, 55 and 72 to 74;

(i) the polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63; or

(j) the antibody of claim 65.

15 76. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

(d) the nucleic acid of any one of claims 40 to 46;

(e) the polypeptide of claim 59 or 60, or a fusion

20 protein of any one of claims 61 to 63; and

(f) the antibody of claim 65.

77. A diagnostic kit comprising instructions for use and a component selected from any one of:

25 (d) the nucleic acid of any one of claims 40 to 46;

(e) the polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63; and

(f) the antibody of claim 65.

30 78. A method for identifying a polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63 which induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

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(a) immunizing a mouse with the polypeptide or fusion protein; and

(b) inoculating the immunized mouse with *Chlamydia*, wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

2001-02-13 10:14:54

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&lt;110&gt; Connaught Laboratories Limited

&lt;120&gt; Chlamydia antigens and corresponding DNA fragments and uses thereof

&lt;130&gt; 77813-5

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&lt;150&gt; 60/114,050

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&lt;170&gt; PatentIn Ver. 2.0

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5/55

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 Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys Thr Phe Pro Ser His  
                   55                                  60                                  65

tcc gcg ggg aaa caa acc cat tcc atg atc ggt tgg gtt ccc caa cat 355  
 Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly Trp Val Pro Gln His  
                   70                                  75                                  80                                  85

ttc tct tat gat cct tgt ttt cct atc tca gta aaa gat gtt gtc ctc 403  
 Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val Lys Asp Val Val Leu  
                                   90                                  95                                  100

tca gga aga ttg tct caa ctc tcc tgg cat gga aaa tat aaa aag aaa 451  
 Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly Lys Tyr Lys Lys Lys  
                                   105                                  110                                  115

gat ttt gaa gct gta gat cac gct ttg gat ctt gtt gga ctt tct gac 499  
 Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu Val Gly Leu Ser Asp  
                                   120                                  125                                  130

acc acc acc act gct ttc gcc cat ctc tca gga gga caa atc cag cgt 547  
 Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly Gly Gln Ile Gln Arg  
                                   135                                  140                                  145

gta ctt ctg gca aga gcc tta gcc tcc tac cct gaa att tta att ctt 595  
 Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro Glu Ile Leu Ile Leu  
                                   150                                  155                                  160                                  165

gat gag ccg acg aca aac att gat cct gac aat caa caa aga att tta 643  
 Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn Gln Gln Arg Ile Leu  
                                   170                                  175                                  180

agt atc cta aaa aag ctc aac cgt acg tgc acc att ctt atg gta act 691  
 Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr Ile Leu Met Val Thr  
                                   185                                  190                                  195

cac gat ctt cac cat acg acg aat tac ttt aat aaa gtt ttt tat atg 739  
 His Asp Leu His His Thr Thr Asn Tyr Phe Asn Lys Val Phe Tyr Met  
                                   200                                  205                                  210

aac aaa act ttg cac ttc att ggc aga cac ttc gac ctt aac aga cca 787  
 Asn Lys Thr Leu His Phe Ile Gly Arg His Phe Asp Leu Asn Arg Pro  
                                   215                                  220                                  225

att ttg ttg tca tcc tat aaa aat cag gaa ttt tca tgc tct cct cac 835  
 Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe Ser Cys Ser Pro His  
                                   230                                  235                                  240                                  245

taatccgtga ttcatttccc cttcttattt tacttccac attcctagcg gcattaggag 895

cctccgtagc tggcgcggtt atgggaacct atatcgttgt aaaacgtatt gtttc 950



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gcg act cta tat caa agc aat gga gag aaa ctt ctg tta gct ttg gac 595  
 Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu Leu Ala Leu Asp  
 150 155 160 165

caa ctc aat gag gaa att ctt acg att acc tcc aaa gcg aaa caa cgc 643  
 Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser Lys Ala Lys Gln Arg  
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cat att tta gtt tcc cat gga gcc ttt ggg tat ttt tgc cgt gat tac 691  
 His Ile Leu Val Ser His Gly Ala Phe Gly Tyr Phe Cys Arg Asp Tyr  
 185 190 195

aat ttc tct cag cac act ata gag aaa agc agt cat gtt gag cct tct 739  
 Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser His Val Glu Pro Ser  
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cct aaa gat gtg gct cgc gta ttt cgt gac att gaa cag tac aaa att 787  
 Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile Glu Gln Tyr Lys Ile  
 215 220 225

tct tct gtg att ctt ctc gaa tac tct gga aga cga agt agt gct atg 835  
 Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg Arg Ser Ser Ala Met  
 230 235 240 245

ctg gca gat cgt ttc cac atg cat act gtg aat ctc gat ccc tat gcg 883  
 Leu Ala Asp Arg Phe His Met His Thr Val Asn Leu Asp Pro Tyr Ala  
 250 255 260

gaa aat gta ctt gta aac tta aaa acc ata gcg acg act ttt tct agt 931  
 Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala Thr Thr Phe Ser Ser  
 265 270 275

tta tgacaatacga aattcttgct gaaggcctag ctttcggtta cggaagcaag 984  
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atagga 1050

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9/55

gga gga atc gct ata aac aat gtc atc att gat ttt agt gaa atc gtt Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val 15 20 25 30	99
cct act aaa gat aat gca aca gta gct cca ccc act ctt aaa tta gta Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val 35 40 45	147
tcg aga act aat gca gat agt aaa gat aag att gat att aca gga act Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr 50 55 60	195
gtg act ctt cta gat cct aat ggc aac tta tat caa aat tct tat ctt Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu 65 70 75	243
ggg gaa gac cgc gat atc act ctt ttc aat ata gac aat tct gca agt Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser 80 85 90	291
ggg gca gtt aca gcc acg aat gtc acc ctt caa ggg aat tta gga gct Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala 95 100 105 110	339
aaa aaa gga tat tta gga acc tgg aat ttg gat cca aat tcc tcg ggt Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly 115 120 125	387
tca aaa att att cta aaa tgg acc ttt gac aaa tac ctg cgc tgg ccc Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro 130 135 140	435
tac atc cct aga gac aac cac ttc tac atc aac tct att tgg gga gca Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala 145 150 155	483
caa aac tct tta gtg act gtg aac caa ggg atc tta ggg aac atg ttg Gln Asn Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu 160 165 170	531
aac aat gca agg ttt gaa gat cct gct ttc aac aac ttc tgg gct tcg Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser 175 180 185 190	579
gct ata gga tct ttc ctt agg aaa gaa gta tct cga aat tct gac tca Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser 195 200 205	627
ttc acc tat cat ggc aga ggc tat acc gct gct gtg gat gcc aaa cct Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro 210 215 220	675
cgc caa gaa ttt att tta gga gct gcc ttc agt cag gtt ttt ggt cac Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His 225 230 235	723

10/55

gcc gag tct gaa tat cac ctt gac aac tat aag cat aaa ggc tca ggt 771  
Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly  
240 245 250

cac tct aca caa gca tct ctt tat gct ggc aat atc ttc tat ttt cct 819  
His Ser Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro  
255 260 265 270

gcg ata cgg tct cgg cct att cta ttc caa ggt gtg gcg acc tat ggt 867  
Ala Ile Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly  
275 280 285

tat atg caa cat gac acc aca acc tac tat cct tct att gaa gaa aaa 915  
Tyr Met Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys  
290 295 300

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Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe  
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agt gtg gat ctt aaa gaa cct caa cct cac tct aca gca agg ctt acc 1011  
Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr  
320 325 330

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Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr  
335 340 345 350

gag cta gac tat gat cct aga tct ttc tct gca tgc tct tat gga aac 1107  
Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn  
355 360 365

tta gca att cct act gga ttc tct gta gac gga gca tta gct tgg cgt 1155  
Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg  
370 375 380

gag att att cta tat aat aaa gta tca gct gcg tac ctg cct gtg att 1203  
Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile  
385 390 395

ctc agg aat aat cca aaa gcg acc tat gaa gtt ctc tct aca aaa gaa 1251  
Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu  
400 405 410

aag ggc aac gta gtc aac gtt ctc cct aca aga aac gca gct cgt gca 1299  
Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala  
415 420 425 430

gag gtg agc tct caa att tat ctt gga agt tac tgg aca ctc tac ggc 1347  
Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly  
435 440 445

acg tat act att gat gct tca atg aat act tta gtg caa atg gcc aac 1395  
Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn  
450 455 460

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 Gly Gly Ile Arg Phe Val Phe  
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tgaggatacag gagagagtgg gattcgaacc cacgggtacgc gttaacgcac acacgctttc 1506

caagcgtgct ccttaagcca ctccggacatc tctccatatt tata 1550

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 Met Arg Phe Ser Leu  
 1 5

tgc gga ttt cct cta gtt ttt tct ttt aca ttg ctc tca gtc ttc gac 163  
 Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu Leu Ser Val Phe Asp  
 10 15 20

act tct ttg agt gct act acg att tct tta acc cca gaa gat agt ttt 211  
 Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr Pro Glu Asp Ser Phe  
 25 30 35

cat gga gat agt cag aat gca gaa cgt tct tat aat gtt caa gct ggg 259  
 His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr Asn Val Gln Ala Gly  
 40 45 50

gat gtc tat agc ctt act ggt gat gtc tca ata tct aac gtc gat aac 307  
 Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile Ser Asn Val Asp Asn  
 55 60 65

tct gca tta aat aaa gcc tgc ttc aat gtg acc tca gga agt gtg acg 355  
 Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr Ser Gly Ser Val Thr  
 70 75 80 85

ttc gca gga aat cat cat ggg tta tat ttt aat aat att tcc tca gga 403  
 Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn Asn Ile Ser Ser Gly  
 90 95 100

act aca aag gaa ggg gct gta ctt tgt tgc caa gat cct caa gca acg 451  
 Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln Asp Pro Gln Ala Thr  
 105 110 115

gca cgt ttt tct ggg ttc tcc acg ctc tct ttt att cag agc ccc gga 499  
 Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe Ile Gln Ser Pro Gly  
 120 125 130

12/55

gat att aaa gaa cag gga tgt ctc tat tca aaa aat gca ctt atg ctc Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys Asn Ala Leu Met Leu 135 140 145	547
tta aac aat tat gta gtg cgt ttt gaa caa aac caa agt aag act aaa Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn Gln Ser Lys Thr Lys 150 155 160 165	595
ggc gga gct att agt ggg gcg aat gtt act ata gta ggc aac tac gat Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile Val Gly Asn Tyr Asp 170 175 180	643
tcc gtc tct ttc tat cag aat gca gcc act ttt gga ggt gct atc cat Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe Gly Gly Ala Ile His 185 190 195	691
tct tca ggt ccc cta cag att gca gta aat cag gca gag ata aga ttt Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln Ala Glu Ile Arg Phe 200 205 210	739
gca caa aat act gcc aag aat ggt tct gga ggg gct ttg tac tcc gat Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly Ala Leu Tyr Ser Asp 215 220 225	787
ggc gat att gat att gat cag aat gct tat gtt cta ttt cga gaa aat Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val Leu Phe Arg Glu Asn 230 235 240 245	835
gag gca ttg act act gct ata ggt aag gga ggg gct gtc tgt tgt ctt Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly Ala Val Cys Cys Leu 250 255 260	883
ccc act tca gga agt agt act cca gtt cct att gtg act ttc tct gac Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile Val Thr Phe Ser Asp 265 270 275	931
aat aaa cag tta gtc ttt gaa aga aac cat tcc ata atg ggt ggc gga Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser Ile Met Gly Gly Gly 280 285 290	979
gcc att tat gct agg aaa ctt agc atc tct tca gga ggt cct act cta Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser Gly Gly Pro Thr Leu 295 300 305	1027
ttt atc aat aat ata tca tat gca aat tgc caa aat tta ggt gga gct Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln Asn Leu Gly Gly Ala 310 315 320 325	1075
att gcc att gat act gga ggg gag atc agt tta tca gca gag aaa gga Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu Ser Ala Glu Lys Gly 330 335 340	1123
aca att aca ttc caa gga aac cgg acg agc tta ccg ttt ttg aat ggc Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu Pro Phe Leu Asn Gly 345 350 355	1171

13/55

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 360 365 370

gga tac tct ata gaa ttt tat gat cct att act tct gaa gca gat ggg 1267  
 Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr Ser Glu Ala Asp Gly  
 375 380 385

tct acc caa ttg aat atc aac gga gat cct aaa aat aaa gag tac aca 1315  
 Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys Asn Lys Glu Tyr Thr  
 390 395 400 405

ggg acc ata ctc ttt tct gga gaa aag agt cta gca aac gat cct agg 1363  
 Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu Ala Asn Asp Pro Arg  
 410 415 420

gat ttt aaa tct aca atc cct cag aac gtc aac ctg tct gca gga tac 1411  
 Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn Leu Ser Ala Gly Tyr  
 425 430 435

tta gtt att aaa gag ggg gcc gaa gtc aca gtt tca aaa ttc acg cag 1459  
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 440 445 450

tct cca gga tcg cat tta gtt tta gat tta gga acc aaa ctg ata gcc 1507  
 Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly Thr Lys Leu Ile Ala  
 455 460 465

tct aag gaa gac att gcc atc aca ggc ctc gcg ata gat ata gat agc 1555  
 Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala Ile Asp Ile Asp Ser  
 470 475 480 485

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 490 495 500

aaa cag ata tcc gtg acg gac tct ata gaa ctt atc tcg cct act ggc 1651  
 Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu Ile Ser Pro Thr Gly  
 505 510 515

aat gcc tat gaa gat ctc aga atg aga aat tca cag acg ttc cct ctg 1699  
 Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser Gln Thr Phe Pro Leu  
 520 525 530

ctc tct tta gag cct gga gcc ggg ggt agt gtg act gta act gct gga 1747  
 Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val Thr Val Thr Ala Gly  
 535 540 545

gat ttc cta ccg gta agt ccc cat tat ggt ttt caa ggc aat tgg aaa 1795  
 Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe Gln Gly Asn Trp Lys  
 550 555 560 565



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tta gct tgg aca gga act gga aac aaa gtt gga gaa ttc ttc tgg gat 1843  
 Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly Glu Phe Phe Trp Asp  
 570 575 580

aaa ata aat tat aag cct aga cct gaa aaa gaa gga aat tta gtt cct 1891  
 Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly Asn Leu Val Pro  
 585 590 595

aat atc ttg tgg ggg aat gct gta gat gtc aga tcc tta atg cag gtt 1939  
 Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg Ser Leu Met Gln Val  
 600 605 610

caa gag acc cat gca tcg agc tta cag aca gat cga ggg ctg tgg atc 1987  
 Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp Arg Gly Leu Trp Ile  
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gat gga att ggg aat ttc ttc cat gta tct gcc tcc gaa gac aat ata 2035  
 Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala Ser Glu Asp Asn Ile  
 630 635 640 645

agg tac cgt cat aac agc ggt gga tat gtt cta tct gta aat aat gag 2083  
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 650 655 660

atc aca cct aag cac tat act tcg atg gca ttt tcc caa ctc ttt agt 2131  
 Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe Ser Gln Leu Phe Ser  
 665 670 675

aga gac aag gac tat gcg gtt tcc aac aac gaa tac aga atg tat tta 2179  
 Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu Tyr Arg Met Tyr Leu  
 680 685 690

gga tcg tat ctc tat caa tat aca acc tcc cta ggg aat att ttc cgt 2227  
 Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu Gly Asn Ile Phe Arg  
 695 700 705

tat gct tcg cgt aac cct aat gta aac gtc ggg att ctc tca aga agg 2275  
 Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly Ile Leu Ser Arg Arg  
 710 715 720 725

ttt ctt caa aat cct ctt atg att ttt cat ttt ttg tgt gct tat ggt 2323  
 Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe Leu Cys Ala Tyr Gly  
 730 735 740

cat gcc acc aat gat atg aaa aca gac tac gca aat ttc cct atg gtg 2371  
 His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala Asn Phe Pro Met Val  
 745 750 755

aaa aac agc tgg aga aac aat tgt tgg gct ata gag tgc gga ggg agc 2419  
 Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile Glu Cys Gly Gly Ser  
 760 765 770

atg cct cta ttg gta ttt gag aac gga aga ctt ttc caa ggt gcc atc 2467  
 Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu Phe Gln Gly Ala Ile  
 775 780 785

15/55

cca ttt atg aaa cta caa tta gtt tat gct tat cat gga gat ttc aaa 2515  
 Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr His Gly Asp Phe Lys  
 790 795 800 805

gag acg act gca gat ggc cgt aga ttt agt aat ggg agt tta aca tcg 2563  
 Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn Gly Ser Leu Thr Ser  
 810 815 820

att tct gta cct cta ggc ata cgc ttt gag aag ctg gca ctt tct cag 2611  
 Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys Leu Ala Leu Ser Gln  
 825 830 835

gat gta ctc tat gac ttt agt ttc tcc tat att cct gat att ttc cgt 2659  
 Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile Pro Asp Ile Phe Arg  
 840 845 850

aag gat ccc tca tgt gaa gct gct ctg gtg att agc gga gac tcc tgg 2707  
 Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile Ser Gly Asp Ser Trp  
 855 860 865

ctt gtt ccg gca gca cac gta tca aga cat gct ttt gta ggg agt gga 2755  
 Leu Val Pro Ala Ala His Val Ser Arg His Ala Phe Val Gly Ser Gly  
 870 875 880 885

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 Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu Leu Leu Cys Arg Gly  
 890 895 900

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 Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr Asn Ile Asn Cys Gly  
 905 910 915

agc aaa ttt cgt ttt tagaagggtt ccattgcctg tgtggttccg gatcttaact 2906  
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&lt;211&gt; 1328

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&lt;213&gt; Chlamydia pneumoniae

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;400&gt; 7

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agcaaccaag caaagaaaagg tgggtgggggtt tatcttgaag atg ccc tca tcc tgg 115  
 Met Pro Ser Ser Trp  
 1 5

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aaa agg tta tta cag gtt ctg tct cac aaa ata gca gct aca gaa agt 163  
 Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile Ala Ala Thr Glu Ser  
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ggt ggg ggt atc tac gct aag gat att caa cta caa gct cta cct gga 211  
 Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu Gln Ala Leu Pro Gly  
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 Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr Ser Leu Thr Thr Ser  
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acc aat ata tct gga acc ttt ggc att aca gga aac tct gtt atc aat 355  
 Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly Asn Ser Val Ile Asn  
 70 75 80 85

aca gcg aca tcc cag gat gca gat ata caa ggt ggg ggc att tat gca 403  
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 90 95 100

acc acg tct ctc tca ata aat caa tgt aat aca ccc att cta ttt agc 451  
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 105 110 115

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 120 125 130

ggt ggg gct atc ttc tcc gct gca gta act atc gag aat aac tct cag 547  
 Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile Glu Asn Asn Ser Gln  
 135 140 145

ccc att att ttc tta aat aat tcc gca aag tgg gaa gca act aca gca 595  
 Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr Thr Ala  
 150 155 160 165

gca act gca gga aat aaa gat agc tgt gga gga gcc att gca gct aac 643  
 Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala Ala Asn  
 170 175 180

tct gtt act tta aca aat aac cct gaa ata acc ttt aaa gga aat tat 691  
 Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys Gly Asn Tyr  
 185 190 195

gca gaa act gga gga gcg att ggc tgt att gat ctt act aat ggc tca 739  
 Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu Thr Asn Gly Ser  
 200 205 210

cct ccc cgt aaa gtc tct att gca gac aac ggt tct gtc ctt ttt caa 787  
 Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly Ser Val Leu Phe Gln  
 215 220 225

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gac aac tct gcg tta aat cgc gga ggc gct atc tat gga gag act atc 835  
 Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile Tyr Gly Glu Thr Ile  
 230 235 240 245

gat atc tcc agg aca ggt gcg act ttc atc ggt aac tct tca aaa cat 883  
 Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly Asn Ser Ser Lys His  
 250 255 260

gat gga agt gca att tgc tgt tca aca gcc cta act ctt gcg cca aac 931  
 Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu Thr Leu Ala Pro Asn  
 265 270 275

tcc caa ctt atc ttt gaa aac aat aag gtt acg gaa acc aca gcc act 979  
 Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr Glu Thr Thr Ala Thr  
 280 285 290

aca aaa gct tcc ata aat aat tta gga gct gca att tat gga aat aat 1027  
 Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala Ile Tyr Gly Asn Asn  
 295 300 305

gag act agt gac gtc act atc tct tta tca gct gag aat gga agt att 1075  
 Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala Glu Asn Gly Ser Ile  
 310 315 320 325

ttc ttt aaa aac aat cta tgc aca gca aca aac aaa tac tgc agt att 1123  
 Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn Lys Tyr Cys Ser Ile  
 330 335 340

gct gga aac gta aaa ttt aca gca ata gaa gct tca gca ggg aaa gct 1171  
 Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala  
 345 350 355

ata tct ttc tat gat gca gtt aac gtt cca cca aag aaa caa ttg ctc 1219  
 Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro Lys Lys Gln Leu Leu  
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aag agc taaattaaat gaaaaagcga caagtacang gacgtttcta ttttctgggg 1275  
 Lys Ser  
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	Met	Lys	Tyr	Ser	Leu	
	1				5	
cct tgg cta ctt acc tct tcg gct tta gtt ttc tcc cta cat cca cta						163
Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe Ser Leu His Pro Leu						
atg gct gct aac acg gat ctc tca tca tcc gat aac tat gaa aat ggt						211
Met Ala Ala Asn Thr Asp Leu Ser Ser Asp Asn Tyr Glu Asn Gly						
agt agt ggt agc gca gca ttc act gcc aag gaa act tcg gat gct tca						259
Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu Thr Ser Asp Ala Ser						
gga act acc tac act ctc act agc gat gtt tct att acg aat gta tct						307
Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser Ile Thr Asn Val Ser						
gca att act cct gca gat aaa agc tgt ttt aca aac aca gga gga gca						355
Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr Asn Thr Gly Gly Ala						
ttg agt ttt gtt gga gct gat cac tca ttg gtt ctg caa acc ata gcg						403
Leu Ser Phe Val Gly Ala Asp His Ser Leu Val Leu Gln Thr Ile Ala						
ctt acg cat gat ggt gct gca att aac aat acc aac aca gct ctt tct						451
Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr Asn Thr Ala Leu Ser						
ttc tca gga ttc tcg tca ctc tta atc gac tca gct cca gca aca gga						499
Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser Ala Pro Ala Thr Gly						
act tcg ggc ggc aag ggt gct att tgt gtg aca aat aca gag gga ggt						547
Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr Asn Thr Glu Gly Gly						
act gcg act ttt act gac aat gcc agt gtc acc ctc caa aaa aat act						595
Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr Leu Gln Lys Asn Thr						
tca gaa aaa gat gga gct gca gtt tct gcc tac agc atc gat ctt gct						643
Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr Ser Ile Asp Leu Ala						
aag act acg aca gca gct ctc tta gat caa aat act agc aca aaa aat						691
Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn Thr Ser Thr Lys Asn						
ggc ggg gcc ctc tgt agt aca gca aac act aca gtc caa gga aac tca						739
Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr Val Gln Gly Asn Ser						

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gga acg gtg acc ttc tcc tca aat act gct aca gat aaa ggt ggg ggg	787
Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr Asp Lys Gly Gly Gly	
215 220 225	
atc tac tca aaa gaa aag gat agc acg cta gat gcc aat aca gga gtc	835
Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp Ala Asn Thr Gly Val	
230 235 240 245	
gtt acc ttc aaa tct aat act gca aag acg ggg ggt gct tgg agc tct	883
Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly Gly Ala Trp Ser Ser	
250 255 260	
gat gac aat ctt gct ctt acc ggc aac act caa gta ctt ttt cag gaa	931
Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln Val Leu Phe Gln Glu	
265 270 275	
aat aaa aca acc ggc tca gca gca cag gca aat aac ccg gaa ggt tgt	979
Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn Asn Pro Glu Gly Cys	
280 285 290	
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Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala Thr Asp Lys Thr Gly	
295 300 305	
tta gcc att tct cag aat caa gaa atg agc ttc act agt aat aca aca	1075
Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe Thr Ser Asn Thr Thr	
310 315 320 325	
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Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys Cys Thr Leu Asp Gly	
330 335 340	
aac aca act ctt acc ttc gat cag aat act gcg aca gca gga tgt ggc	1171
Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala Thr Ala Gly Cys Gly	
345 350 355	
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Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser Leu Lys Gly Ser Thr	
360 365 370	
gga acc gtg acc ttc agc aca aat aca gca aag aca ggc ggc tta	1267
Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly Gly Ala Leu	
375 380 385	
tat tct aaa gga aac agc tcg ctg act gga aat acc aac ctg ctc ttt	1315
Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn Thr Asn Leu Leu Phe	
390 395 400 405	
tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca aat caa gag	1363
Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala Asn Gln Glu	
410 415 420	
ggg tgc ggt ggg gca atc cta gcc ttt att gat tca gga tcc gta agc	1411
Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp Ser Gly Ser Val Ser	
425 430 435	

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gat aaa aca gga cta tgc att gca aac aac caa gaa gtc agc ctc act 1459  
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agt aat gct gca aca gta agt ggt ggt gcg atc tat gct acc aaa tgt 1507  
 Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala Thr Lys Cys  
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act cta act gga aac ggc tcc ctg acc ttt gac ggc aat act gct gga 1555  
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 Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Thr Leu Thr  
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gga agt aca gga acc gtg acc ttc agc aca aat aca gca aag aca ggc 1651  
 Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly  
 505 510 515

ggc gcc tta tat tct aaa ggc aac aac tct ctg tct ggt aat acc aac 1699  
 Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu Ser Gly Asn Thr Asn  
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ctg ctc ttt tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca 1747  
 Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala  
 535 540 545

aat caa gag ggt tgc ggt ggg gca atc cta tgc ttt ctt gag tca gca 1795  
 Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser Phe Leu Glu Ser Ala  
 550 555 560 565

tct gta agt act aaa aaa gga ctc tgg att gaa gat aac gaa aac gtg 1843  
 Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu Asp Asn Glu Asn Val  
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agt ctc tct ggt aat act gca aca gta agt ggc ggt gcg atc tat gcg 1891  
 Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala  
 585 590 595

acc aag tgt gct ctg cat gga aac acg act ctt acc ttt gat ggc aat 1939  
 Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp Gly Asn  
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 Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe  
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act ctt acg gga agt acg gga acc gtg acc ttc agc aca aat aca gca 2035  
 Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala  
 630 635 640 645

aag aca gca ggg gct cta cat act aaa gga aat act tcc ttt acc aaa 2083  
 Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn Thr Ser Phe Thr Lys  
 650 655 660

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aat aag gct ctt gta ttt tct gga aat tca gca aca gca aca gca aca 2131  
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 665 670 675

aca act aca gat caa gaa ggt tgt ggt gga gcg atc ctc tgt aat atc 2179  
 Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala Ile Leu Cys Asn Ile  
 680 685 690

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tat gct cct aag tgt gta atc tca ggc agt gaa tcc ata aac ttt gat 2323  
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 745 750 755

tcg att aca gct aac ggt cct gtc tcc ttt acc aat aat tct gga ggc 2419  
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 760 765 770

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 775 780 785

gct att gat ggg gat att act ttc tca ggg aac cga gcg act gag gga 2515  
 Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn Arg Ala Thr Glu Gly  
 790 795 800 805

act tca act ccc aac tcg atc cat tta ggt gcc agg ggc aag atc act 2563  
 Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala Arg Gly Lys Ile Thr  
 810 815 820

aag ctt gca gca gct cct ggt cat acg att tat ttt tat gat cct att 2611  
 Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr Phe Tyr Asp Pro Ile  
 825 830 835

acg atg gaa gct cct gca tct gga gga aca ata gag gag tta gtc atc 2659  
 Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile Glu Glu Leu Val Ile  
 840 845 850

aat cct gtt gtc aaa gct att gtt cct cct ccc caa cca aaa aat ggt 2707  
 Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro Gln Pro Lys Asn Gly  
 855 860 865

cct ata tagaagaaaa acgaatgctc ttgttaaggc tcaagagtaa aaaattctaa 2763  
 Pro Ile  
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agggtattctc tcaatagggt ctgaagtgtc gccgtagaat tcataaatat etc 2816

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 Met Thr Asn Ser Ile  
 1 5

ttc ata tca aag ttt gga tgt tta tgc gac cca ttt gtc tca gca ttt 163  
 Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro Phe Val Ser Ala Phe  
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tat ccc act gcg cta tgt tgt tcc tta tca gga aat gaa gtc cct aac 211  
 Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly Asn Glu Val Pro Asn  
 25 30 35

ctc gcc tct tgt cag atg tct aga aaa gac atc tct gct ttc cac acg 259  
 Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile Ser Ala Phe His Thr  
 40 45 50

tct cca agc ttc cgt ctg aat gta act cca gag ccc ttg gtt tcc tcc 307  
 Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu Pro Leu Val Ser Ser  
 55 60 65

ttt cgt ccc tct aat ctt ctt aat gga ttc ggt cac gat ata acc cag 355  
 Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly His Asp Ile Thr Gln  
 70 75 80 85

gac atc aca att aca gga aac tct atc aat tct gtt ata gat tat aac 403  
 Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser Val Ile Asp Tyr Asn  
 90 95 100

tac cac tac gag gat gga ggc att ctt gca tgt aaa aat ttg ttc att 451  
 Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys Lys Asn Leu Phe Ile  
 105 110 115

tct gaa aat aaa gga aac tta agt ttt gaa agg aat agc tcc cac agt 499  
 Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg Asn Ser Ser His Ser  
 120 125 130

tct gga ggg gct ctc tac agt gtt cgg gaa tgc tgg att tct aag aat 547  
 Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys Trp Ile Ser Lys Asn  
 135 140 145

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cag aac tac tgc ttt att tca aat gcg gct tcc tta gct act act aca 595  
 Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser Leu Ala Thr Thr Thr  
 150 155 160 165

act tca gga ttt ggt ggg gct ata cat gca cta gat agc tat att aca 643  
 Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile Thr  
 170 175 180

aat aac tta gga gaa gga caa ttc tta gat aat gtc tct aaa aat aga 691  
 Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn Arg  
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ggt cct atc gtt atc aag aaa aat caa aca tta gaa gat tcc agc ttt 787  
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 215 220 225

gga gga ggc atc ttc tgc aga gcc gta aat ata gaa agg aat tat caa 835  
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 265 270 275

agc aat cac tcc gca tcc tca att aac aca gca tca gga aaa cta tat 979  
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 280 285 290

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 295 300 305

ccc aaa ggt ctt atc ttt aac aat aaa acg gca gca ctt agc ggc gga 1075  
 Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala Ala Leu Ser Gly Gly  
 310 315 320 325

gta tac aca cga gat ctt tca tct tcc aaa ata acg gtc cgc aca gca 1123  
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 330 335 340

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 Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala Leu Ile Asn Leu Ser  
 345 350 355

ggt ata gga agt act cct caa aat ttc ttc ctc tct gca gac tac ggc 1219  
 Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu Ser Ala Asp Tyr Gly  
 360 365 370

24/55

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 375 380 385

gga tat aga aat gca ctc tat gct gct ccg ggg att aac tta aaa cta 1315  
 Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly Ile Asn Leu Lys Leu  
 390 395 400 405

gga gca aga cag ggt tat aaa att ctc ttt tat gat cct ata gat cac 1363  
 Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr Asp Pro Ile Asp His  
 410 415 420

gat cag acg aca aca gat cct ata gta ttt aat tat gaa ccc cat cac 1411  
 Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn Tyr Glu Pro His His  
 425 430 435

ctt ggc acc gtg ttg ttt tcc gga atc aat gta gat tct aac gca aca 1459  
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 440 445 450

aat cca ttg aac ttc cta tca aaa ttt tct aac tct tca cga ctt gaa 1507  
 Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn Ser Ser Arg Leu Glu  
 455 460 465

agg ggt gtg ctc gct att gaa gat ccg gct gct att tct tgc aaa acc 1555  
 Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala Ile Ser Cys Lys Thr  
 470 475 480 485

cta tcg caa act ggg ggc att cta cgt tta gga aac gca gca tta atc 1603  
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 490 495 500

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 Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe Asn Ala Ile Ala Ile  
 505 510 515

aat ctt cct tct att tta caa tca gaa gcc tca gct cca aag ttc tgg 1699  
 Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser Ala Pro Lys Phe Trp  
 520 525 530

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 Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser Glu Asp Thr Ser Ser  
 535 540 545

act atc act ctc tca gga ccc ttg act ttt cta aac gat gaa aat gaa 1795  
 Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu Asn Asp Glu Asn Glu  
 550 555 560 565

aac ccc tat gat agc tta gat ctc tct gaa cct cga aag gat atc ccc 1843  
 Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro Arg Lys Asp Ile Pro  
 570 575 580

cct cct cta cct cct cga tgt gac tgc aaa aac atc gat act tcg aat 1891  
 Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys Ile Asp Thr Ser Asn  
 585 590 595

25/55

ctc att gta gaa gcc atg aac tta gat gag cac tat gga tat cag gga 1939  
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atc tgg tct ccc tat tgg atg gaa act acg act aca aca agc tct aca 1987  
 Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr Thr Ser Ser Thr  
 615 620 625

gta ccg gaa cag acc aat aca aac cac agg cag ctc tac gta gac tgg 2035  
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 630 635 640 645

act cct gta gga tac cgc cct aac ccg gaa cgt cac gga gaa ttt att 2083  
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 650 655 660

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 Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp Leu Glu Ala Ser Leu  
 680 685 690

caa gga ctc ggg ctt cta att aac caa cat aat cgc gag gga cgc aaa 2227  
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ggc ttc cga aac cat act acg ggc tat gca gca aca acc tca gca aaa 2275  
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aaa act aga gaa cgt caa tct cca agt acg act tcc tcc cac aac tac 2371  
 Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr Ser Ser His Asn Tyr  
 745 750 755

ttt gca gga ctc cgc ttc gac agt ctc ctc ttc agg gac ttc atc tct 2419  
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 760 765 770

aca ggg cta tcc cta ggt tat agc tac gga gat cac cat atg ctt tgc 2467  
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 775 780 785

cac tat aca gaa atc tta aaa ggg tcg tcc aaa gcc ttc ttt aat aac 2515  
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 790 795 800 805

cac act ttg gta gcc tct cta gac tgc aca ttc tta cca gct aga atc 2563  
 His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe Leu Pro Ala Arg Ile  
 810 815 820

26/55

acc cgc act ctc gaa ctc cag ccc ttt atc agt gcc att gct ctg cgc 2611  
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 825 830 835

tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc 2659  
 Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe  
 840 845 850

cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt 2707  
 His Pro Lys His Pro Leu Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg  
 855 860 865

tct gaa tgg aaa act tca cat cat atc ccc atg cta tgg act acg gaa 2755  
 Ser Glu Trp Lys Thr Ser His His Ile Pro Met Leu Trp Thr Thr Glu  
 870 875 880 885

ata tcc tac gta cct acc cta tac aga aaa aat cca gaa atg ttc acg 2803  
 Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn Pro Glu Met Phe Thr  
 890 895 900

aca cta ctc atc agc aat gga aca tgg aca aca caa gca act ccc gtc 2851  
 Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr Gln Ala Thr Pro Val  
 905 910 915

tcc tat aat tcc gta gct gca aaa ata aaa aat act tcc caa ctt ttc 2899  
 Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe  
 920 925 930

tca aga gta acc tta tcc tta gat tat tca gct caa gtc tcc tcg tca 2947  
 Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser  
 935 940 945

act gta ggt caa tac ctt aaa gct gag agt cat tgc aca ttt 2989  
 Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His Cys Thr Phe  
 950 955 960

taaccacaaa gaaaacatca aggaataaac agtgcaaaat aacagatccc ttagtaaato 3049

ttctcttcttt gtgtggagcct taatttttagg taaaactaca ata 3092

<210> 10  
 <211> 1745  
 <212> DNA  
 <213> Chlamydia pneumoniae

<220>  
 <221> CDS  
 <222> (101)..(1642)

<400> 10  
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 attaaagtgt cttcaacctt attgatttaa cgaggaaacc atg acc ata ctt cga 115

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Met Thr Ile Leu Arg  
1 5

aat ttt ctt acc tgc tgc gct tta ttc ctc gct ctc cct gca gca gca 163  
Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala Leu Pro Ala Ala Ala  
10 15 20

caa gtt gta tat ctt cat gaa agt gat ggt tat aac ggt gct atc aat 211  
Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn  
25 30 35

aat aaa agc tta gaa cct aaa att acc tgt tat cca gaa gga act tct 259  
Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser  
40 45 50

tac atc ttt cta gat gac gtg agg att tcc aac gtt aag cat gat caa 307  
 Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln  
 55 60 65

gaa gat gct ggg gtt ttt ata aat cga tct ggg aat ctt ttt ttc atg 355  
Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met  
70 75 80 85

ggc aac cgt tgc aac ttc act ttt cac aac ctt atg acc gag ggt ttt 403  
Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu Met Thr Glu Gly Phe  
90 95 100

ggc gct gcc att tcg aac cgc gtt gga gac acc act ctc act ctc tct 451  
Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr Thr Leu Thr Leu Ser  
105 110 115

aat ttt tct tac tta gcg ttc acc tca gca cct cta cta cct caa gga 499  
Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly  
120 125 130

caa gga gcg att tat agt ctt ggt tcc gtg atg atc gaa aat agt gag 547  
Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met Ile Glu Asn Ser Glu  
135 140 145

gaa gtc act ttc tgt ggg aac tac tct tgc tgg agt gga gct gcg att 595  
Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile  
150 155 160 165

tat act ccc tac ctt tta ggt tct aag gcg agt cgt cct tca gta aat 643  
Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser Arg Pro Ser Val Asn  
170 175 180

ctc agc ggg aac cgc tac ctg gtg ttt aga gac aat gtg agc caa gtt 691  
Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp Asn Val Ser Gln Val  
185 190 195

tat ggc ggc gcc ata tct acc cac aat ctc aca ctc acg act cga gga 739  
Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr Leu Thr Thr Arg Gly  
200 205 210

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cct tcg tgt ttt gaa aat aat cat gct tat cat gac gtg aat agt aat Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His Asp Val Asn Ser Asn 215 220 225	787
gga gga gcc att gcc att gct cct gga gga tcg atc tct ata tcc gtg Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser Ile Ser Ile Ser Val 230 235 240 245	835
aaa agc gga gat ctc atc ttc aaa gga aat aca gca tca caa gac gga Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly 250 255 260	883
aat aca ata cac aac tcc atc cat ctg caa tct gga gca cag ttt aag Asn Thr Ile His Asn Ser Ile His Leu Gln Ser Gly Ala Gln Phe Lys 265 270 275	931
aac cta cgt gct gtt tca gaa tcc gga gtt tat ttc tat gat cct ata Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile 280 285 290	979
agc cat agc gag tcg cat aaa att aca gat ctt gta atc aat gct cct Ser His Ser Glu Ser His Lys Ile Thr Asp Leu Val Ile Asn Ala Pro 295 300 305	1027
gaa gga aag gaa act tat gaa gga aca att agc ttc tca gga cta tgc Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys 310 315 320 325	1075
ctg gat gat cat gaa gtt tgt gcg gaa aat ctt act tcc aca atc cta Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu 330 335 340	1123
caa gat gtc aca tta gca gga gga act ctc tct cta tcg gat ggg gtt Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser Leu Ser Asp Gly Val 345 350 355	1171
acc ttg caa ctg cat tct ttt aag cag gaa gca agc tct acg ctt act Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr 360 365 370	1219
atg tct cca gga acc act ctg ctc tgc tca gga gat gct cgg gtt cag Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly Asp Ala Arg Val Gln 375 380 385	1267
aat ctg cac atc ctg att gaa gat acc gac aac ttt gtt cct gta agg Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn Phe Val Pro Val Arg 390 395 400 405	1315
att cgc gcc gag gac aag gat gct ctt gtc tca tta gaa aaa ctt aaa Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser Leu Glu Lys Leu Lys 410 415 420	1363
gtt gcc ttt gag gct tat tgg tcc gtc tat gac ttt cct caa ttt aag Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp Phe Pro Gln Phe Lys 425 430 435	1411

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gaa gcc ttt acg att cct ctt ctt gaa ctt cta ggg cct tct ttt gac 1459  
 Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp  
 440 445 450

agt ctt etc cta ggg gag acc act ttg gag aga acc caa gtc aca aca 1507  
 Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg Thr Gln Val Thr Thr  
 455 460 465

gag aat gac gcc gtt cga ggt ttc tgg tcc cta agc tgg gaa gag tac 1555  
 Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu Ser Trp Glu Glu Tyr  
 470 475 480 485

ccc cct tct ctg gat aaa gac aga agg atc aca cca act aag aaa act 1603  
 Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr  
 490 495 500

gtt ttc etc act tgg aat cct gag atc act tct acg cca taatctctaa 1652  
 Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser Thr Pro  
 505 510

gtctacacta taattaaggg aatccccctt aagaagattt tgggacctat ctgtattcag 1712

agataggtcc ctctatgac acatgttcac gag 1745

<210> 11

<211> 1100

<212> DNA

<213> Chlamydia pneumoniae

<220>

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<222> (101)..(967)

<400> 11

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cagattttcc aaaacttcta taaatggaaa taaagagcct atg gga atc tct cta 115  
 Met Gly Ile Ser Leu  
 1 5

cca gag ctt ttt tcc aac cta ggt tct gct tac tta gat tat atc ttt 163  
 Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr Leu Asp Tyr Ile Phe  
 10 15 20

caa cat cct cgg gcc tat gtt tgg tca gtt ttt ctt ctt tta tta gcc 211  
 Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe Leu Leu Leu Ala  
 25 30 35

cgt ctg ctt cct att ttt gct gta gct ccc ttc tta gga gca aag etc 259  
 Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu  
 40 45 50

ttt ccc tcc cct att aaa atc ggg att agt ctc tct tgg ctt gca atc 307  
 Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu Ser Trp Leu Ala Ile  
 55 60 65



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atc ttt cca aaa gtc ttg gcg gat acg cag atc aca aat tac atg gat 355  
 Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile Thr Asn Tyr Met Asp  
 70 75 80 85

aac aat ctc ttt tat gtt tta ctt gtg aag gag atg atc ata ggc att 403  
 Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu Met Ile Ile Gly Ile  
 90 95 100

gtg ata ggc ttt gtt tta gca ttt ccc ttt tat gct gca caa tgc gca 451  
 Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr Ala Ala Gln Ser Ala  
 105 110 115

gga tct ttc atc act aac caa caa ggg att cag ggt tta gag ggc gcg 499  
 Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln Gly Leu Glu Gly Ala  
 120 125 130

aca tcc ctg att tcc att gag cag acc tct ccg cat ggc att tta tac 547  
 Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro His Gly Ile Leu Tyr  
 135 140 145

cat tac ttc gtg act att att ttt tgg tta gtg ggt ggt cac cgt att 595  
 His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val Gly Gly His Arg Ile  
 150 155 160 165

gta atc tct ttg tta ttg caa act ctt gaa gtc att ccg atc cat agt 643  
 Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val Ile Pro Ile His Ser  
 170 175 180

ttc ttt cct gcc gag atg atg agc tta agt gcc ccg att tgg att act 691  
 Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala Pro Ile Trp Ile Thr  
 185 190 195

atg atc aag atg tgc cag ctc tgt ctc gtg atg acc ata cag ctg agt 739  
 Met Ile Lys Met Cys Gln Leu Cys Leu Val Met Thr Ile Gln Leu Ser  
 200 205 210

gct cct gca gct ttg gcg atg tta atg tcc gac cta ttc tta ggg att 787  
 Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp Leu Phe Leu Gly Ile  
 215 220 225

att aac cgt atg gca cct caa gtt cag gtc atc tac ctc ctc tct gcc 835  
 Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile Tyr Leu Leu Ser Ala  
 230 235 240 245

ctt aag gct ttc atg ggt ctt ctc ttt ctc acc ctg gcg tgg tgg ttc 883  
 Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr Leu Ala Trp Trp Phe  
 250 255 260

ata att aag cag ata gat tat ttc act ctt gct tgg ttc aaa gaa gtc 931  
 Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala Trp Phe Lys Glu Val  
 265 270 275

ccc att atg ctc cta ggt tcc aac cct caa gta ctc taatcccccta 977  
 Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val Leu  
 280 285



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tta atc aac tgc cta ggt ctt tat tct att gct aaa gag ttg aag cac   547
Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys Glu Leu Lys His
    135                      140                      145

att ctg gat aag gtt gtg att gaa cga gtg aag aat gct ctc tcc cct   595
Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro
    150                      155                      160                      165

aca gag aaa ctc ttt ctt acc tac tgc caa tct cat ccg atg aaa cat   643
Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His
                      170                      175

tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta   691
Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu
                      185                      190                      195

cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta   739
Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu
                      200                      205                      210

aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat   787
Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp
                      215                      220                      225

gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac   835
Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp
    230                      235                      240                      245

cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa   883
His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys
                      250                      255                      260

gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta   935
Val Leu Val Lys
                      265

tagaaaaata acacg
                                           950

<210> 13
<211> 500
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(385)

<400> 13
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tccaagggct tatgatcagc tttaaataag gacacgtgcc atg tta gca ttt ttc   115
Met Leu Ala Phe Phe
                      1                      5

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gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta 163  
Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu  
10 15 20

tta ctt att ttg att gtt tct gca cct ccc atc atc tta gct tcc ata 211  
Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile  
25 30 35

gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa 259  
Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu  
40 45 50

cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta 307  
Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu  
55 60 65

atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt 355  
Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly  
70 75 80 85

cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct 405  
Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
90 95

ctctaccaga gcttttttcc aacctagggt ctgcttactt agattatata tttcaacatc 465  
ctccggccta tgtttgggtca gttttttctc tttta 500

<210> 14

<211> 552

&lt;212&gt; PRT

<213> Chlamydia pneumoniae

<400> 14

Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser  
1 5 10 15

Val Ser Gly Lys Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp  
20 25 30

Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu  
35 40 45

Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile  
50 55 60

Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr  
65 70 75 80

Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu  
85 90 95

Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu  
100 105 110

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Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala  
 115 120 125  
 Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln  
 130 135 140  
 Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala  
 145 150 155 160  
 Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe  
 165 170 175  
 Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu  
 180 185 190  
 Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe  
 195 200 205  
 Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met  
 210 215 220  
 Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys  
 225 230 235 240  
 Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu  
 245 250 255  
 Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly  
 260 265 270  
 Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala  
 275 280 285  
 Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser  
 290 295 300  
 Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys  
 305 310 315 320  
 Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala  
 325 330 335  
 Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val  
 340 345 350  
 Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala  
 355 360 365  
 Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr  
 370 375 380  
 Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr  
 385 390 395 400

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Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala  
 405 410 415

Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His  
 420 425 430

Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu  
 435 440 445

Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp  
 450 455 460

Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val  
 465 470 475 480

Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr  
 485 490 495

Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly  
 500 505 510

Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu  
 515 520 525

Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met  
 530 535 540

Val Arg Lys Glu Asn Arg Ser Lys  
 545 550

<210> 15  
 <211> 196  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 15  
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 1 5 10 15

Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly  
 20 25 30

Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val  
 35 40 45

Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg  
 50 55 60

Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val  
 65 70 75 80

Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe  
 85 90 95

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His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala  
 100 105 110  
 Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala  
 115 120 125  
 Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu  
 130 135 140  
 Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe  
 145 150 155 160  
 Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val  
 165 170 175  
 Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys  
 180 185 190  
 Ile Ala Arg Val  
 195  
 <210> 16  
 <211> 245  
 <212> PRT  
 <213> Chlamydia pneumoniae  
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 Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser  
 1 5 10 15  
 Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly  
 20 25 30  
 Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu  
 35 40 45  
 Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys  
 50 55 60  
 Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly  
 65 70 75 80  
 Trp Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val  
 85 90 95  
 Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly  
 100 105 110  
 Lys Tyr Lys Lys Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu  
 115 120 125  
 Val Gly Leu Ser Asp Thr Thr Thr Ala Phe Ala His Leu Ser Gly  
 130 135 140  
 Gly Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro  
 145 150 155 160

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Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn  
165 170 175

Gln Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr  
180 185 190

Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn  
195 200 205

Lys Val Phe Tyr Met Asn Lys Thr Leu His Phe Ile Gly Arg His Phe  
210 215 220

Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe  
225 230 235 240

Ser Cys Ser Pro His  
245

&lt;210&gt; 17

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 17

Met His Lys Val Ile Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys  
1 5 10 15

Ser Tyr Gly Asn Asp Val Ile Asp Lys Pro His Val Leu Val Ser Ile  
20 25 30

Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe  
35 40 45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu  
50 55 60

Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg  
65 70 75 80

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln  
85 90 95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys  
100 105 110

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro  
115 120 125

Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys  
130 135 140



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Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu  
 145 150 155 160  
 Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser  
 165 170 175  
 Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr  
 180 185 190  
 Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser  
 195 200 205  
 His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile  
 210 215 220  
 Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg  
 225 230 235 240  
 Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn  
 245 250 255  
 Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala  
 260 265 270  
 Thr Thr Phe Ser Ser Leu  
 275

<210> 18  
 <211> 469  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 18  
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 20 25 30  
 Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg  
 35 40 45  
 Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr  
 50 55 60  
 Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu  
 65 70 75 80  
 Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala  
 85 90 95  
 Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys  
 100 105 110

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Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys  
 115 120 125  
 Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile  
 130 135 140  
 Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn  
 145 150 155 160  
 Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn  
 165 170 175  
 Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile  
 180 185 190  
 Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr  
 195 200 205  
 Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln  
 210 215 220  
 Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu  
 225 230 235 240  
 Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser  
 245 250 255  
 Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile  
 260 265 270  
 Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met  
 275 280 285  
 Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met  
 290 295 300  
 Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val  
 305 310 315 320  
 Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr  
 325 330 335  
 Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu  
 340 345 350  
 Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala  
 355 360 365  
 Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile  
 370 375 380  
 Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg  
 385 390 395 400

40/55

Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly  
 405 410 415

Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val  
 420 425 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr  
 435 440 445

Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly  
 450 455 460

Ile Arg Phe Val Phe  
 465

&lt;210&gt; 19

&lt;211&gt; 922

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 19

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu  
 1 5 10 15

Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr  
 20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr  
 35 40 45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile  
 50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr  
 65 70 75 80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn  
 85 90 95

Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln  
 100 105 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe  
 115 120 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys  
 130 135 140

Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn  
 145 150 155 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile  
 165 170 175

41/55

Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe  
180 185 190

Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln  
195 200 205

Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly  
210 215 220

Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val  
225 230 235 240

Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly  
245 250 255

Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile  
260 265 270

Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser  
275 280 285

Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser  
290 295 300

Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln  
305 310 315 320

Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu  
325 330 335

Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu  
340 345 350

Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys  
355 360 365

Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr  
370 375 380

Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys  
385 390 395 400

Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu  
405 410 415

Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn  
420 425 430

Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val  
435 440 445

Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly  
450 455 460

Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala  
465 470 475 480

42/55

Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys  
 485 490 495  
 Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu  
 500 505 510  
 Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser  
 515 520 525  
 Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val  
 530 535 540  
 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe  
 545 550 555 560  
 Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly  
 565 570 575  
 Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu  
 580 585 590  
 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg  
 595 600 605  
 Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp  
 610 615 620  
 Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala  
 625 630 635 640  
 Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu  
 645 650 655  
 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe  
 660 665 670  
 Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu  
 675 680 685  
 Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu  
 690 695 700  
 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly  
 705 710 715 720  
 Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe  
 725 730 735  
 Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala  
 740 745 750  
 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile  
 755 760 765

43/55

Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu  
 770 775 780  
 Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr  
 785 790 795 800  
 His Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn  
 805 810 815  
 Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys  
 820 825 830  
 Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile  
 835 840 845  
 Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile  
 850 855 860  
 Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala  
 865 870 875 880  
 Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu  
 885 890 895  
 Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr  
 900 905 910  
 Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe  
 915 920  
 <210> 20  
 <211> 375  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 20  
 Met Pro Ser Ser Trp Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile  
 1 5 10 15  
 Ala Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu  
 20 25 30  
 Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr  
 35 40 45  
 Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser  
 50 55 60  
 Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly  
 65 70 75 80  
 Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly  
 85 90 95

44/55

Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr  
 100 105 110  
 Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr  
 115 120 125  
 Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile  
 130 135 140  
 Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser  
 145 150 155 160  
 Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly  
 165 170 175  
 Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr  
 180 185 190  
 Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp  
 195 200 205  
 Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly  
 210 215 220  
 Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile  
 225 230 235 240  
 Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly  
 245 250 255  
 Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu  
 260 265 270  
 Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr  
 275 280 285  
 Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala  
 290 295 300  
 Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala  
 305 310 315 320  
 Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn  
 325 330 335  
 Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala  
 340 345 350  
 Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro  
 355 360 365  
 Lys Lys Gln Leu Leu Lys Ser  
 370 375

45/55

<210> 21  
 <211> 871  
 <212> PRT  
 <213> Chlamydia pneumoniae

&lt;400&gt; 21

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Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe
 1          5          10          15

Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp
          20          25          30

Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu
          35          40          45

Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser
          50          55          60

Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr
 65          70          75          80

Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val
          85          90          95

Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr
100          105          110

Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser
115          120          125

Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr
130          135          140

Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr
145          150          155          160

Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr
165          170          175

Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn
180          185          190

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr
195          200          205

Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr
210          215          220

Asp Lys Gly Gly Gly Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp
225          230          235          240

Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly
245          250          255

Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln
260          265          270

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46/55

Val Leu Phe Gln Glu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn  
 275 280 285  
 Asn Pro Glu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala  
 290 295 300  
 Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe  
 305 310 315 320  
 Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys  
 325 330 335  
 Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala  
 340 345 350  
 Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser  
 355 360 365  
 Leu Lys Gly Ser Thr Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys  
 370 375 380  
 Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn  
 385 390 395 400  
 Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser  
 405 410 415  
 Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp  
 420 425 430  
 Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln  
 435 440 445  
 Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile  
 450 455 460  
 Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp  
 465 470 475 480  
 Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu  
 485 490 495  
 Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn  
 500 505 510  
 Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu  
 515 520 525  
 Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro  
 530 535 540  
 Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser  
 545 550 555 560

47/55

Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu  
 565 570 575  
 Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly  
 580 585 590  
 Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu  
 595 600 605  
 Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr  
 610 615 620  
 Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe  
 625 630 635 640  
 Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn  
 645 650 655  
 Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala  
 660 665 670  
 Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala  
 675 680 685  
 Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr  
 690 695 700  
 Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg  
 705 710 715 720  
 Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu  
 725 730 735  
 Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile  
 740 745 750  
 Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr  
 755 760 765  
 Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly  
 770 775 780  
 Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn  
 785 790 795 800  
 Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala  
 805 810 815  
 Arg Gly Lys Ile Thr Lys Leu Ala Ala Pro Gly His Thr Ile Tyr  
 820 825 830  
 Phe Tyr Asp Pro Ile Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile  
 835 840 845  
 Glu Glu Leu Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro  
 850 855 860

48/55

Gln Pro Lys Asn Gly Pro Ile  
865 870

&lt;210&gt; 22

&lt;211&gt; 963

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 22

Met Thr Asn Ser Ile Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro  
1 5 10 15

Phe Val Ser Ala Phe Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly  
20 25 30

Asn Glu Val Pro Asn Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile  
35 40 45

Ser Ala Phe His Thr Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu  
50 55 60

Pro Leu Val Ser Ser Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly  
65 70 75 80

His Asp Ile Thr Gln Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser  
85 90 95

Val Ile Asp Tyr Asn Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys  
100 105 110

Lys Asn Leu Phe Ile Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg  
115 120 125

Asn Ser Ser His Ser Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys  
130 135 140

Trp Ile Ser Lys Asn Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser  
145 150 155 160

Leu Ala Thr Thr Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu  
165 170 175

Asp Ser Tyr Ile Thr Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn  
180 185 190

Val Ser Lys Asn Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser  
195 200 205

Ile Thr Asp Asn Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu  
210 215 220

Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile  
225 230 235 240

49/55

Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln  
 245 250 255  
 Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys  
 260 265 270  
 Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala  
 275 280 285  
 Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu  
 290 295 300  
 Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala  
 305 310 315 320  
 Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile  
 325 330 335  
 Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala  
 340 345 350  
 Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu  
 355 360 365  
 Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser  
 370 375 380  
 Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly  
 385 390 395 400  
 Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr  
 405 410 415  
 Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn  
 420 425 430  
 Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val  
 435 440 445  
 Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn  
 450 455 460  
 Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala  
 465 470 475 480  
 Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly  
 485 490 495  
 Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe  
 500 505 510  
 Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser  
 515 520 525

50/55

Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser  
530 535 540

Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu  
545 550 555 560

Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro  
565 570 575

Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys  
580 585 590

Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His  
595 600 605

Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr  
610 615 620

Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln  
625 630 635 640

Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg  
645 650 655

His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala  
660 665 670

Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp  
675 680 685

Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn  
690 695 700

Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala  
705 710 715 720

Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe  
725 730 735

Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr  
740 745 750

Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe  
755 760 765

Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp  
770 775 780

His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys  
785 790 795 800

Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe  
805 810 815

Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser  
820 825 830

51/55

Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp  
835 840 845

His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser  
850 855 860

Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met  
865 870 875 880

Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn  
885 890 895

Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr  
900 905 910

Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn  
915 920 925

Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala  
930 935 940

Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His  
945 950 955 960

Cys Thr Phe

&lt;210&gt; 23

&lt;211&gt; 514

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 23

Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala  
1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr  
20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr  
35 40 45

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn  
50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly  
65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu  
85 90 95

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr  
100 105 110

52/55

Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro  
115 120 125

Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met  
130 135 140

Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp  
145 150 155 160

Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser  
165 170 175

Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp  
180 185 190

Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr  
195 200 205

Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His  
210 215 220

Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser  
225 230 235 240

Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr  
245 250 255

Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser  
260 265 270

Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr  
275 280 285

Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu  
290 295 300

Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser  
305 310 315 320

Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu  
325 330 335

Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser  
340 345 350

Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala  
355 360 365

Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly  
370 375 380

Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn  
385 390 395 400

Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser  
405 410 415

53/55

Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp  
420 425 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu  
435 440 445

Gly Pro Ser Phe Asp Ser Leu Leu Gly Glu Thr Thr Leu Glu Arg  
450 455 460

Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu  
465 470 475 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr  
485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser  
500 505 510

Thr Pro

<210> 24

<211> 289

<212> PRT

<213> Chlamydia pneumoniae

<400> 24

Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr  
1 5 10 15

Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe  
20 25 30

Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe  
35 40 45

Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu  
50 55 60

Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile  
65 70 75 80

Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu  
85 90 95

Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr  
100 105 110

Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln  
115 120 125

Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro  
130 135 140



54/55

His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val  
145 150 155 160

Gly Gly His Arg Ile Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val  
165 170 175

Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala  
180 185 190

Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met  
195 200 205

Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp  
210 215 220

Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile  
225 230 235 240

Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr  
245 250 255

Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala  
260 265 270

Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val  
275 280 285

Leu

<210> 25

<211> 265

<212> PRT

<213> Chlamydia pneumoniae

<400> 25

Met Lys His Ser Lys Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn  
1 5 10 15

Leu Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu  
20 25 30

Ser Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr  
35 40 45

Ile Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala  
50 55 60

Trp Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly  
65 70 75 80

Ile Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu  
85 90 95

Leu Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu  
100 105 110

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Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly  
 115 120 125  
 Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala  
 130 135 140  
 Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys  
 145 150 155 160  
 Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser  
 165 170 175  
 His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr  
 180 185 190  
 Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe  
 195 200 205  
 Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe  
 210 215 220  
 Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu  
 225 230 235 240  
 Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu  
 245 250 255  
 Glu Gln Cys Met Lys Val Leu Val Lys  
 260 265  
 <210> 26  
 <211> 95  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 26  
 Met Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr  
 1 5 10 15  
 Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile  
 20 25 30  
 Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala  
 35 40 45  
 Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val  
 50 55 60  
 Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile  
 65 70 75 80  
 Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
 85 90 95

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Figure 1

Restriction enzyme analysis of CPN100686 (RY 54 - SEQ ID NO. 1)

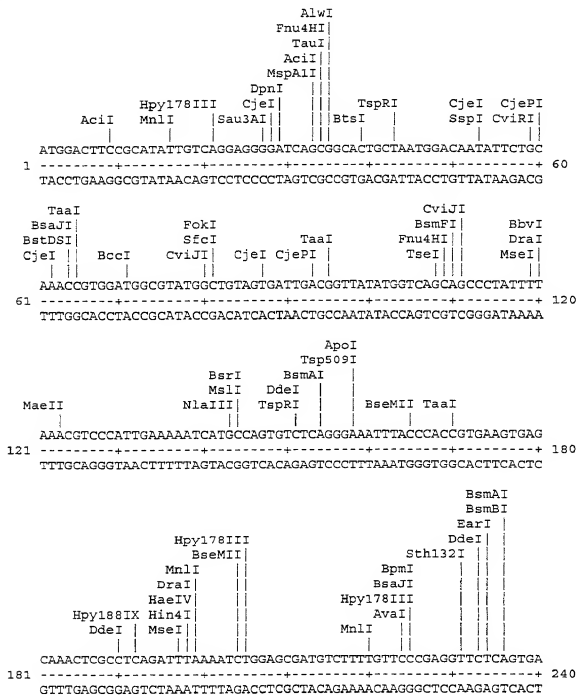
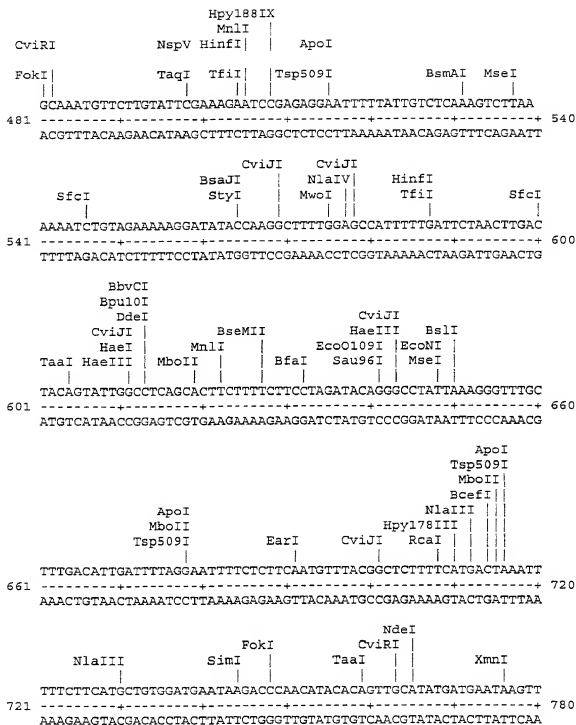


Figure 1 (Continued)

[illegible]

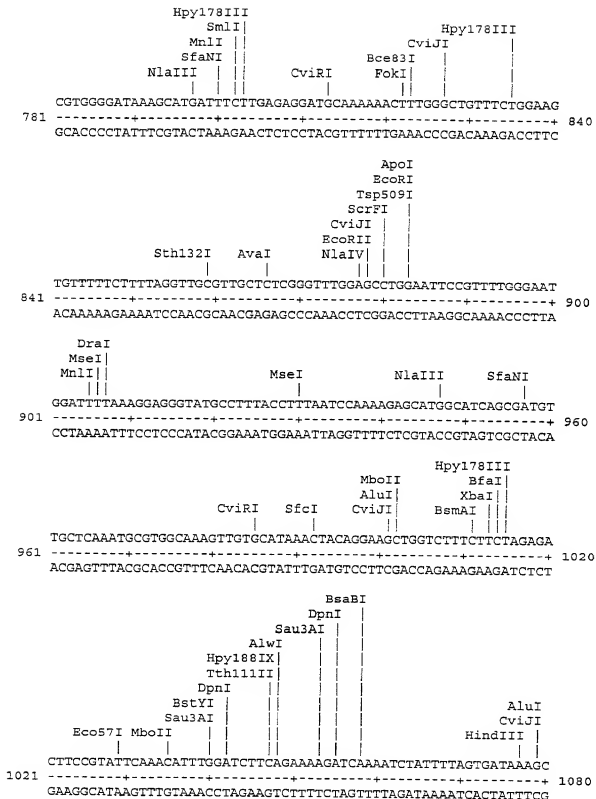
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Figure 1 (continued)



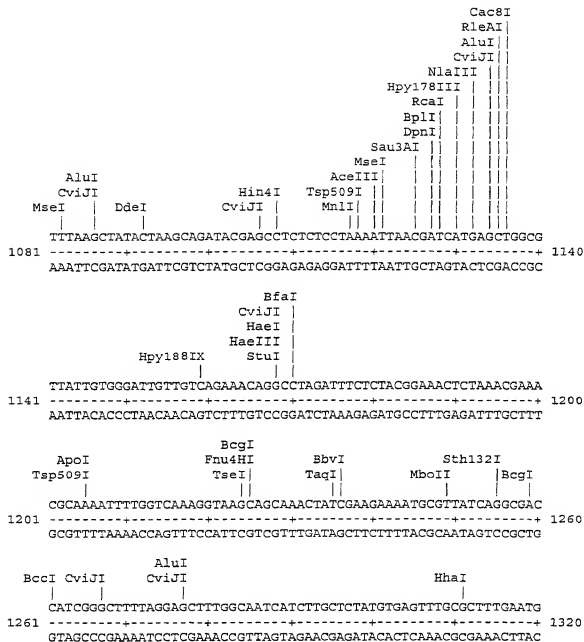
631019987

Figure 1 (continued)



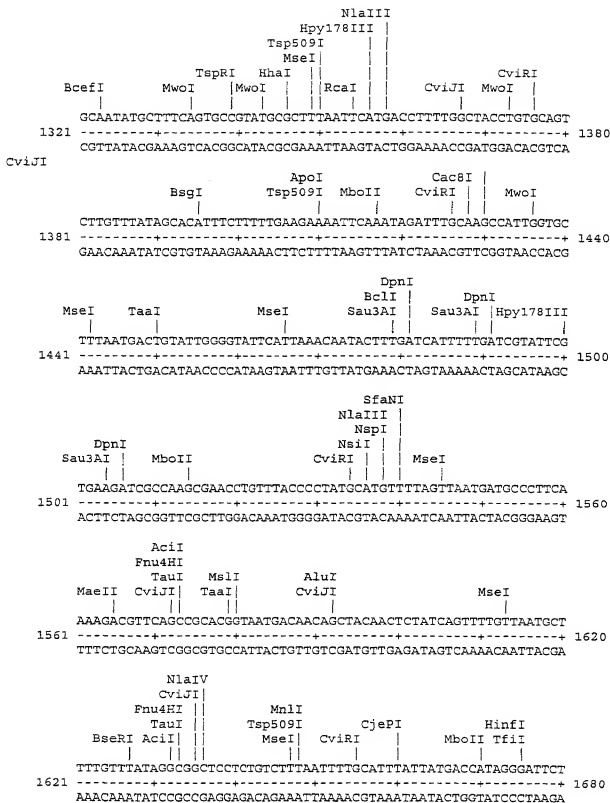
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Figure 1 (continued)



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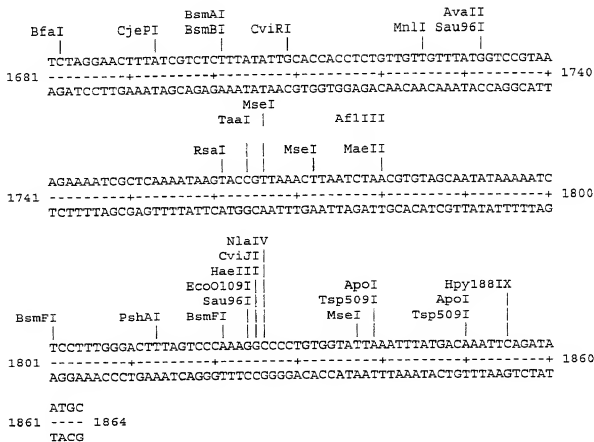
Figure 1 (continued)





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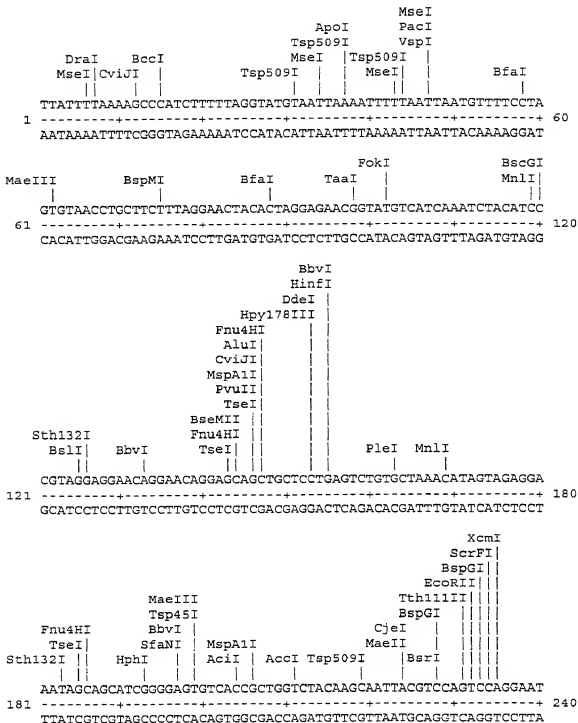
Figure 1 (continued)



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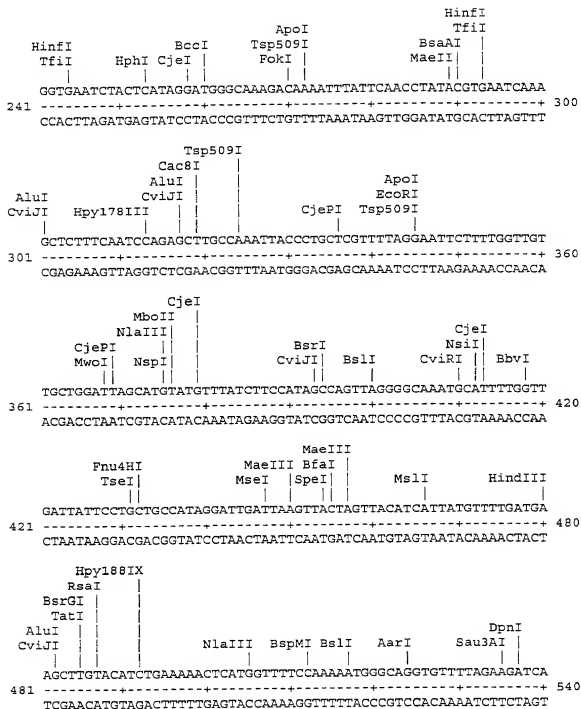
Figure 2

Restriction enzyme analysis of CPN100696 (RY 55 - SEQ ID NO. 2)



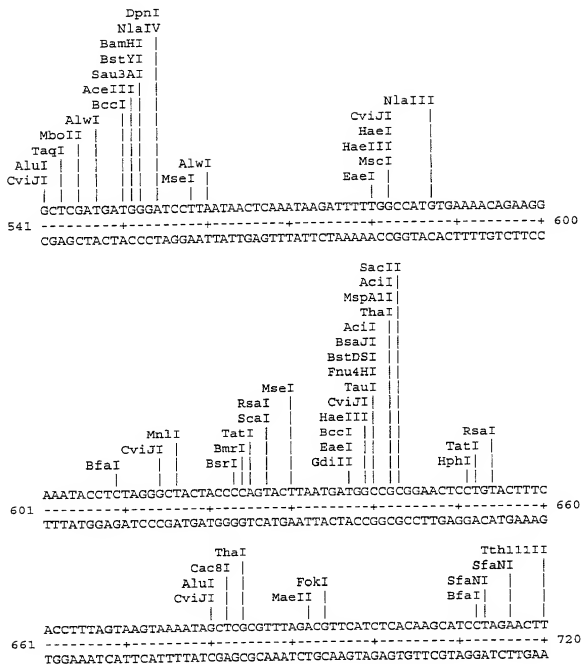
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Figure 2 (continued)



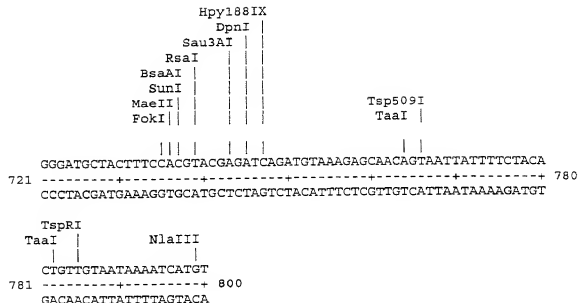
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Figure 2 (continued)



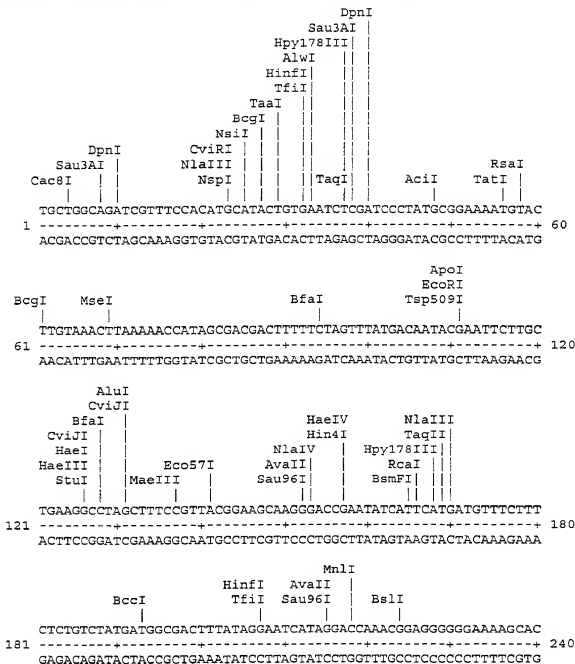
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Figure 2 (continued)



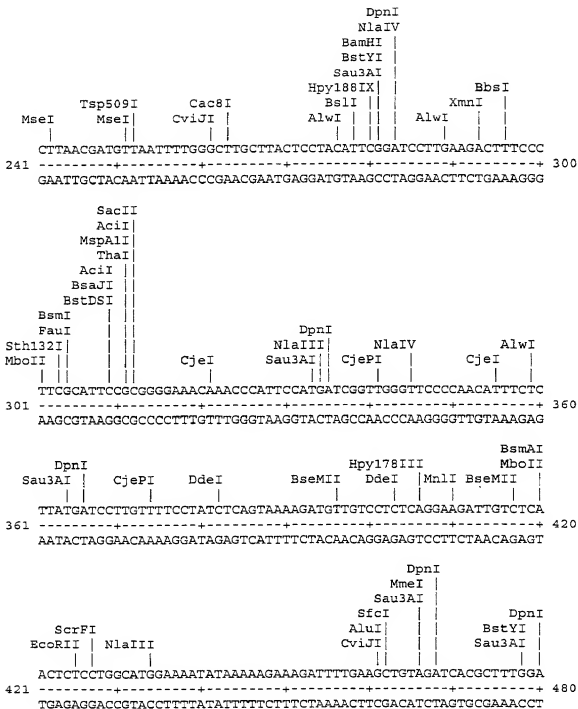
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Figure 3  
Restriction enzyme analysis of CPN100709 (RY 57 - SEQ ID NO. 3)



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Figure 3 (continued)

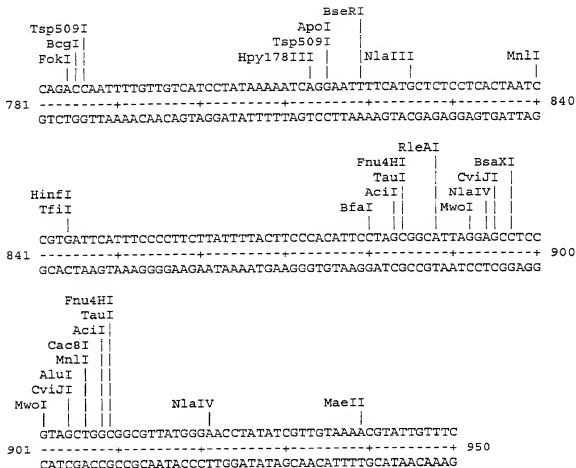






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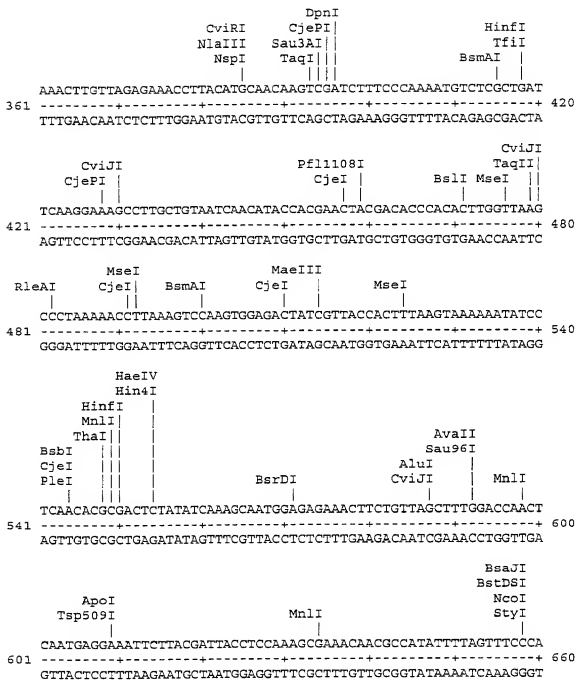
Figure 3 (continued)





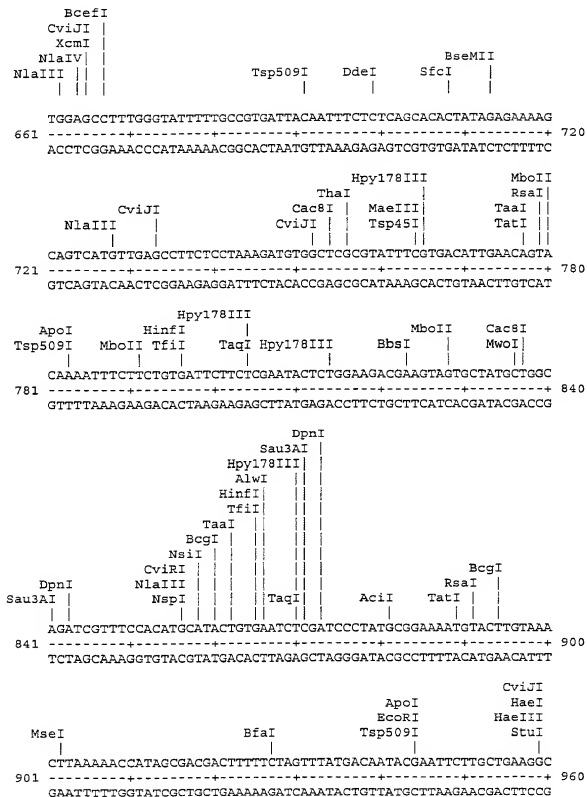
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Figure 4 (continued)



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Figure 4 (continued)



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Figure 4 (continued)

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                                HaeIV      NlaIII
                                Hin4I      TaqII
                                NlaIV      Hpy178III
                                AvaII      RcaI
                                Sau96I      BsmFI
AluI      Eco57I      BfaI      MaeIII
CTAGCTTTCCGTTACGGAAGCAAGGGACCGAATATCATTTCATGATGTTCTTTCTCTGTC
961 -----+ 1020
GATCGAAAGGCAATGCCTTCGTTCCCTGGCTTATAGTAAGTACTACAAAGAAAGAGACAG

                                MnlI
                                HinfI      AvaII
                                TfiI      Sau96I      BslI
                                BccI      MseI
TATGATGGCGACTTTATAGGAATCATAGGACCAAACGGAGGGGGGAAAAGCACCTTAACG
1021 -----+ 1080
ATACTACC3CTGAAATATCCTTAGTATCTCGTTTGCCTCCCCCTTTTCGTGGAATTGC

                                DpnI
                                NlaIV
                                BamHI
                                BstYI
                                Sau3AI
                                Hpy188IX
                                BslI
                                BbsI      BsmI
                                XmnI      Sth132I
                                AlwI      MboII
Tsp509I      Cac8I      CviJI      AlwI
ATGTTAATTTTGGGCTTGCTTACTCCTACATTCGGATCCTTGAAGACTTTCCTTCGCAT
1081 -----+ 1140
TACAATTAACCCGAAACGAATGAGGATGTAAGCCTAGGAACCTCTGAAAGGGAAGCGTA

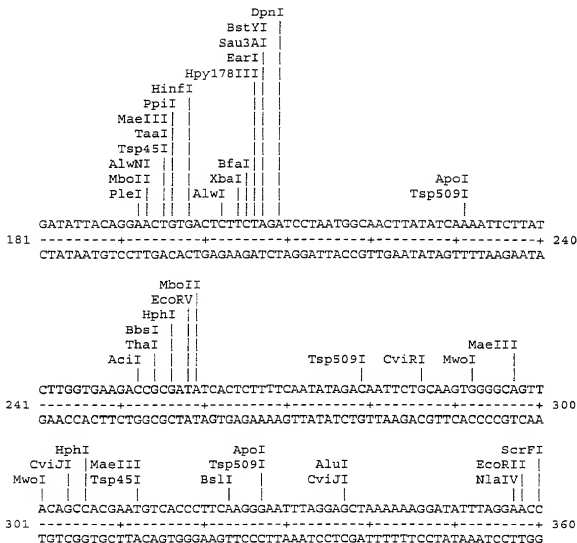
SacII
AciII
MspAII
ThaI
AciII
BsaJI
BstDSI
TCCGCGGGGAAACAAACCCATT
1141 ----- 1162
AGGCGCCCCCTTGTTTGGGTAA

```



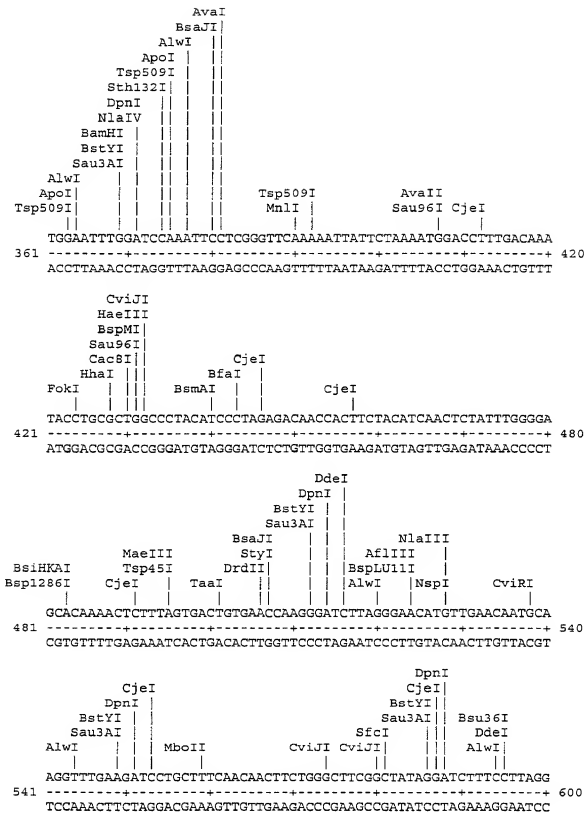
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Figure 5 (continued)



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Figure 5 (continued)

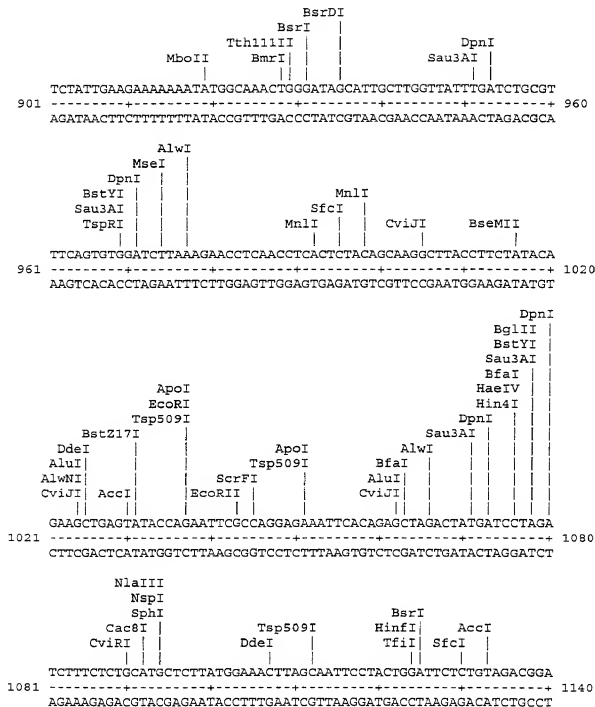






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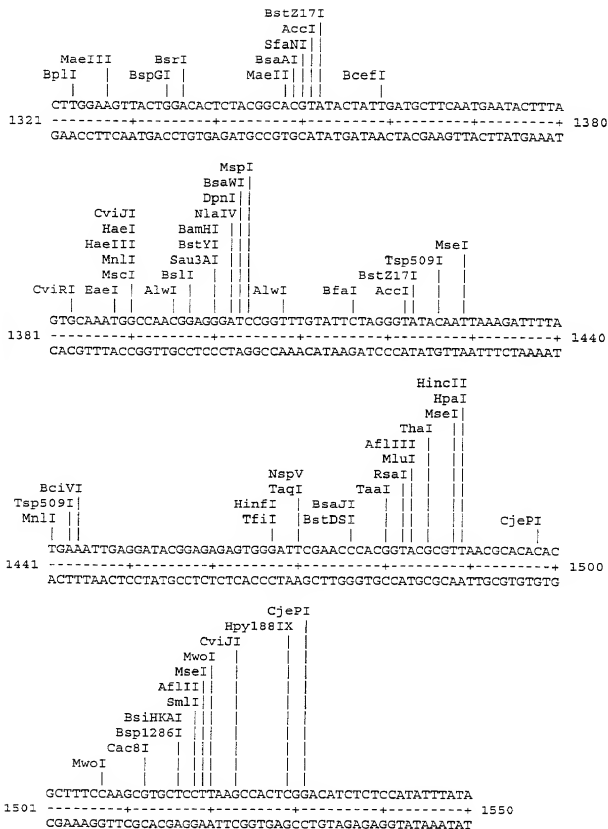
Figure 5 (continued)





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Figure 5 (continued)



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Figure 6

Restriction enzyme analysis of CPN100877 (RY 61 - SEQ ID NO. 6)

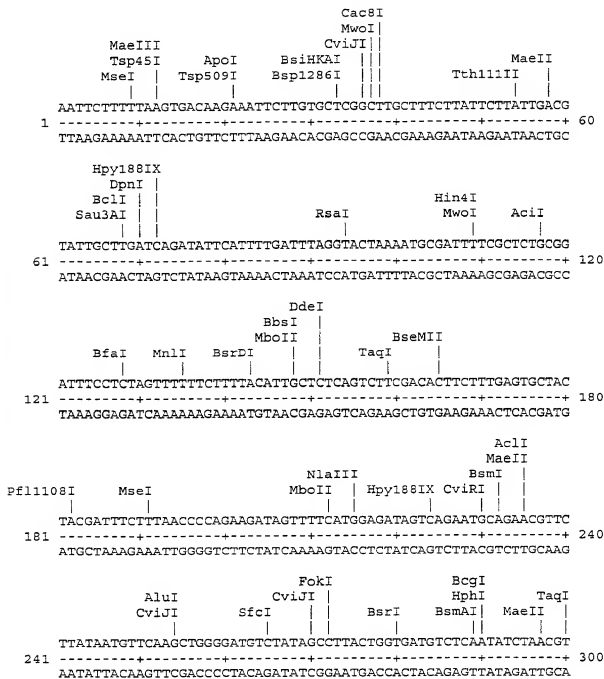
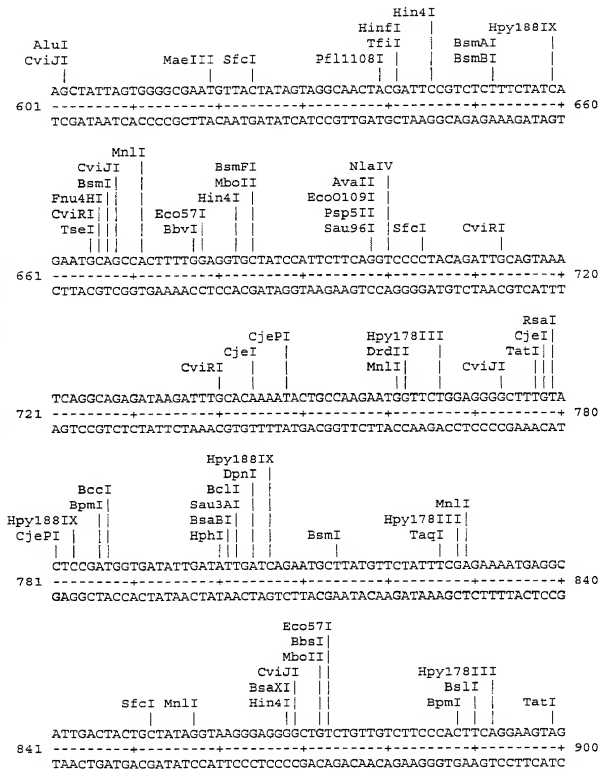


Figure 6 (continued)



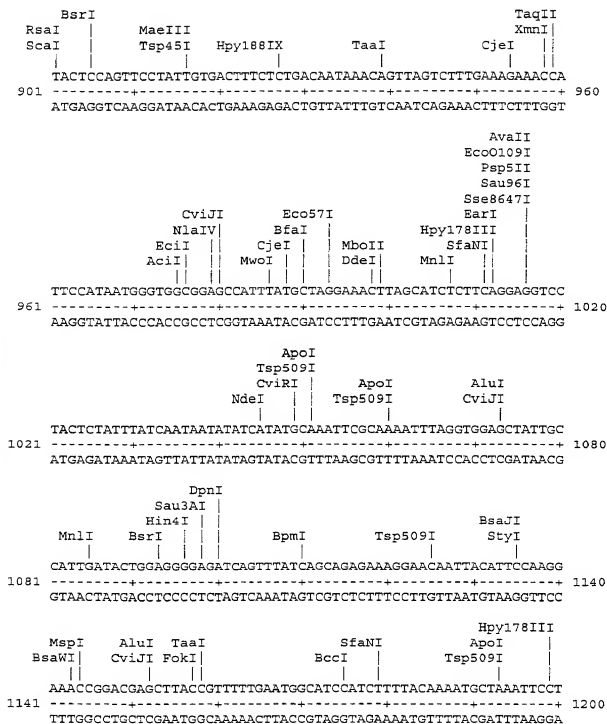
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Figure 6 (continued)



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Figure 6 (continued)





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Figure 6 (continued)

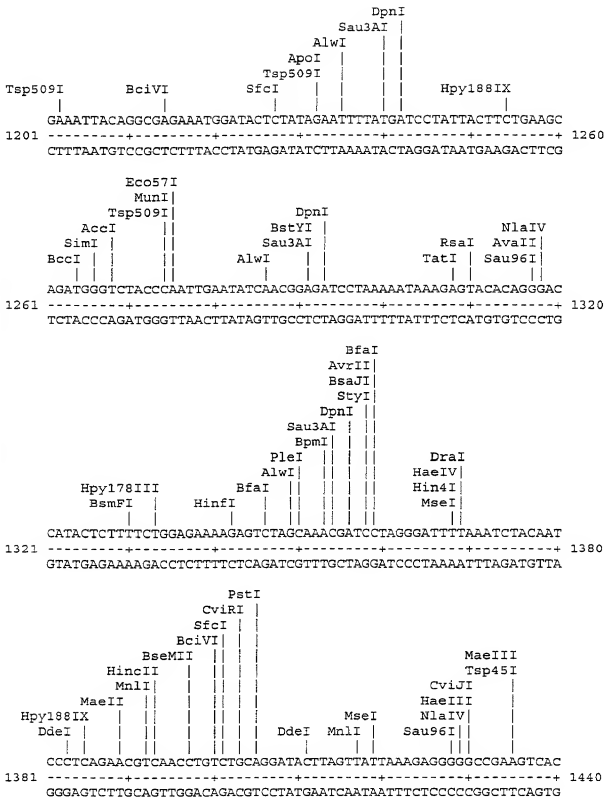
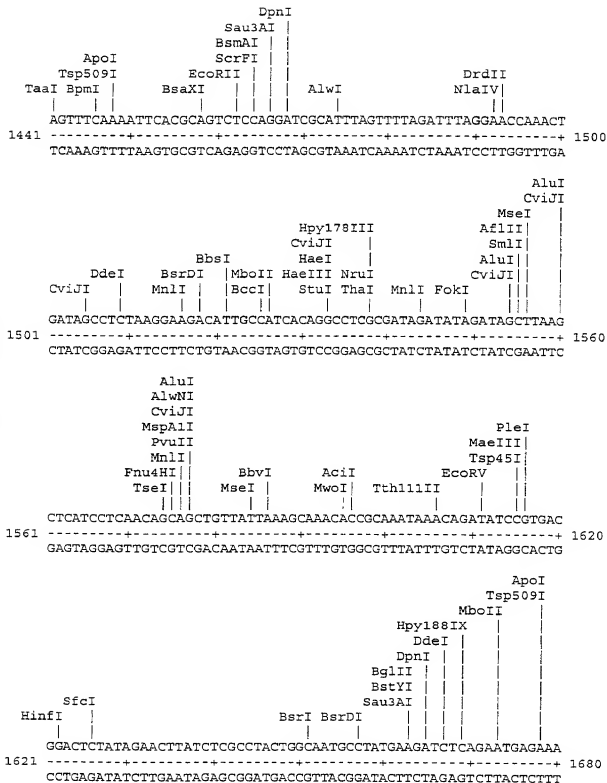


Figure 6 (continued)



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Figure 6 (continued)

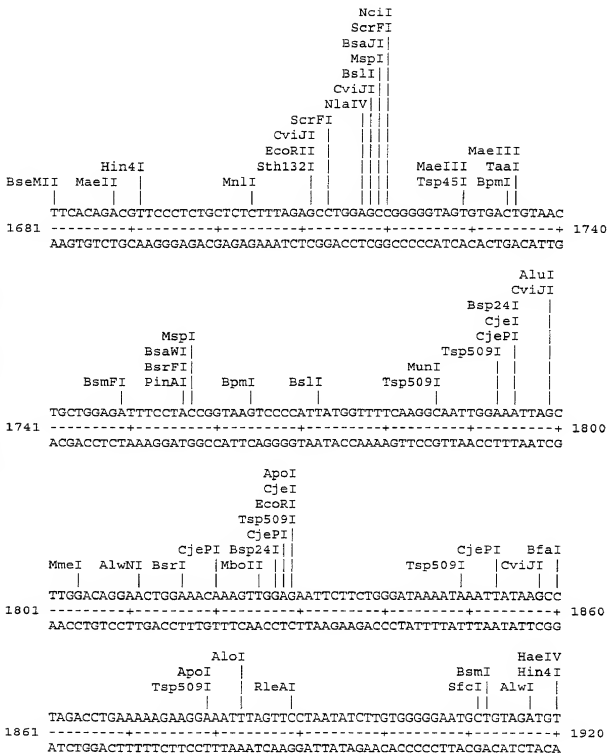
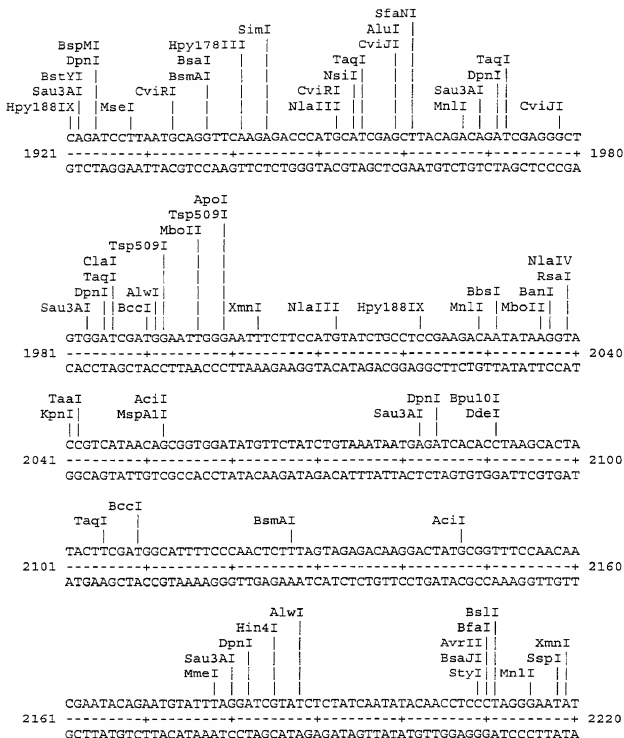
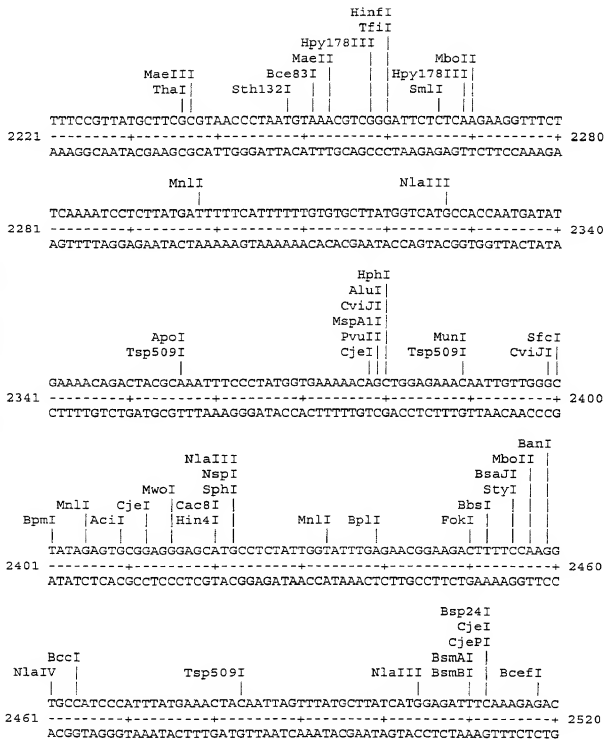


Figure 6 (continued)



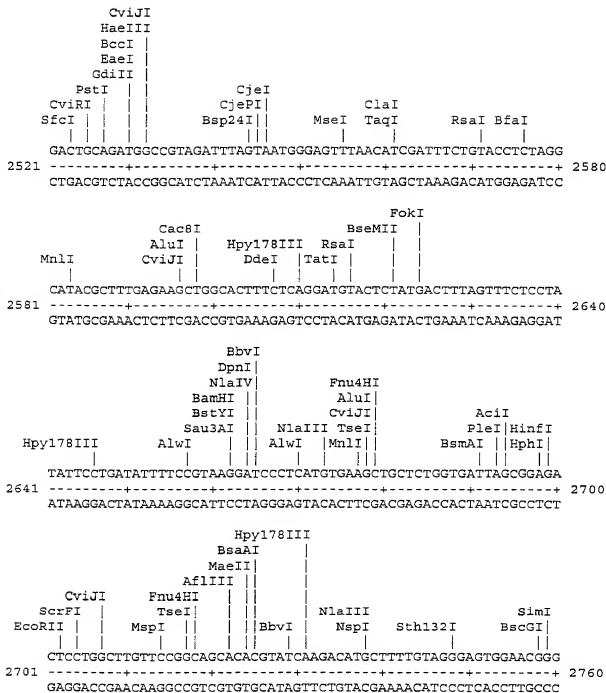
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Figure 6 (continued)



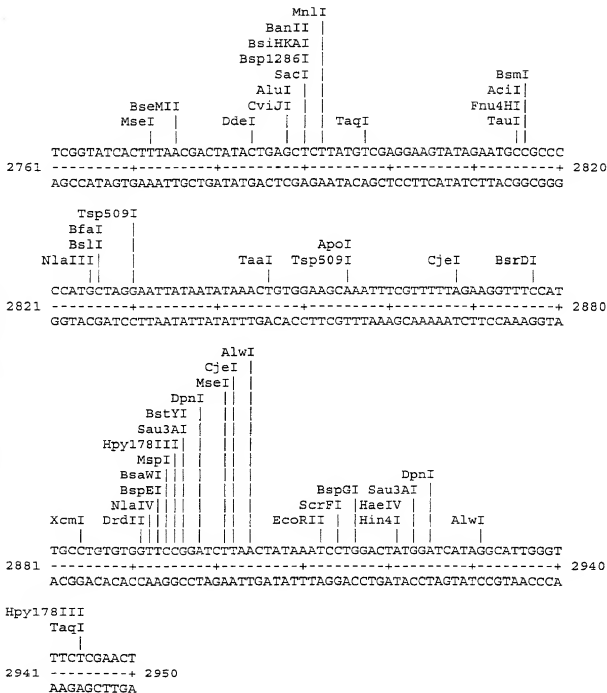
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Figure 6 (continued)



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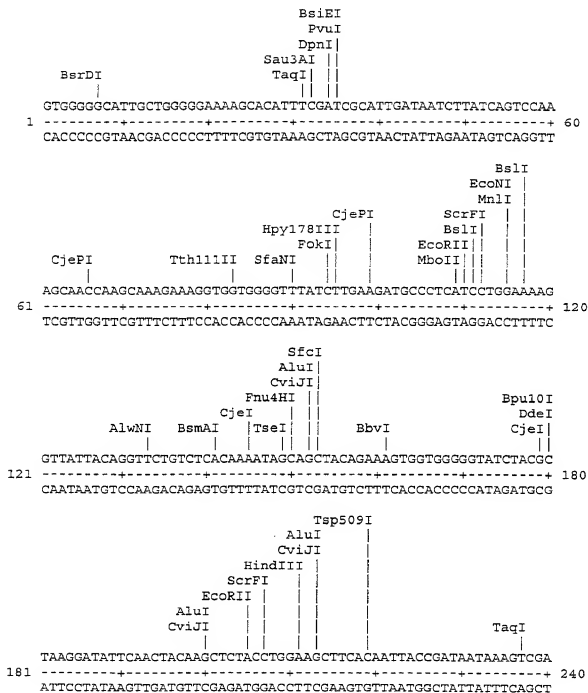
Figure 6 (continued)



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Figure 7

Restriction enzyme analysis of CPN100325 (RY 62 - SEQ ID NO. 7)





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Figure 7 (continued)

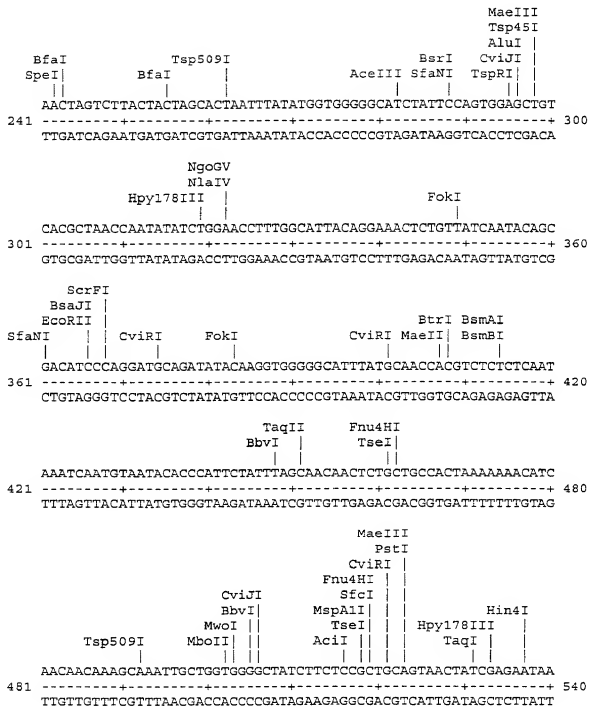


Figure 7 (continued)



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Figure 7 (continued)

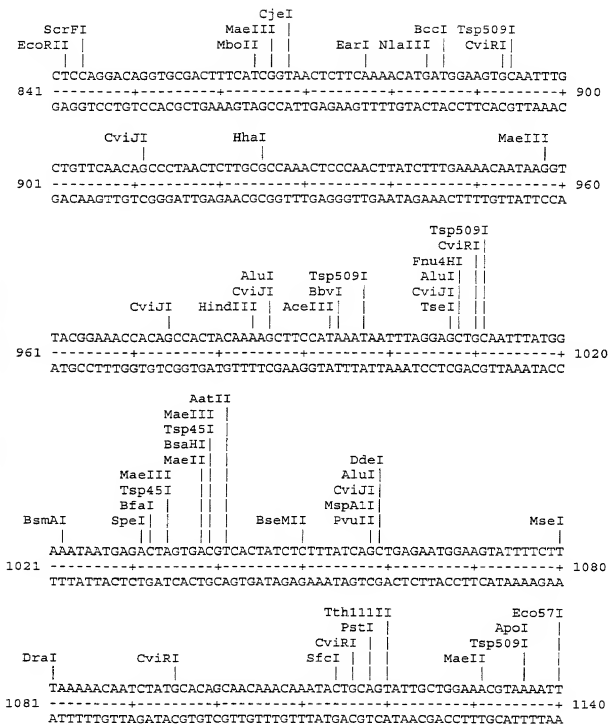


Figure 7 (continued)

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Figure 8

Restriction enzyme analysis of CPN100368 (RY 63 - SEQ ID NO. 8)

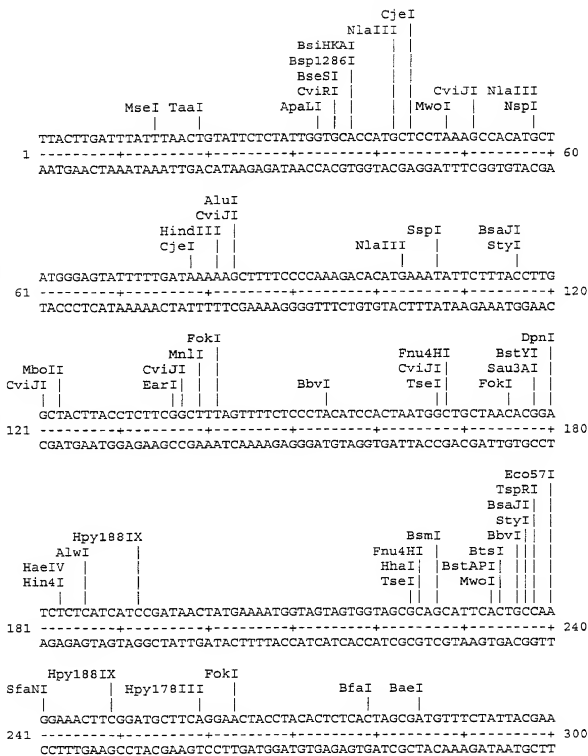
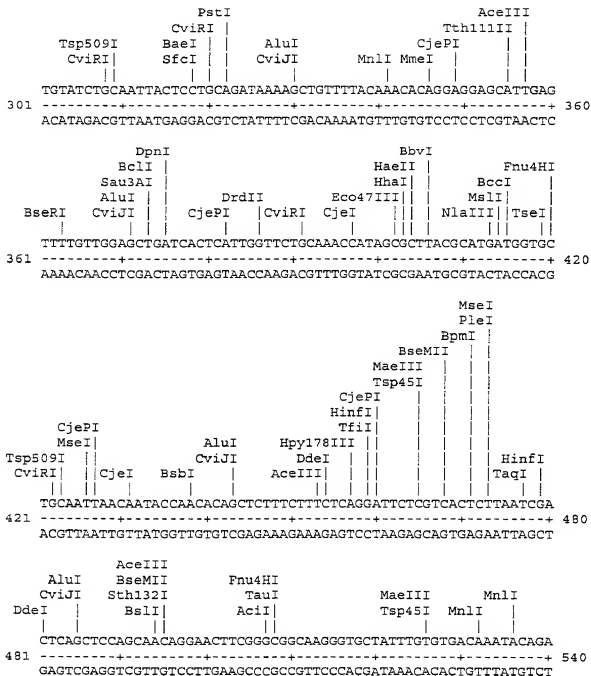


Figure 9 (continued)



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Figure 9 (continued)

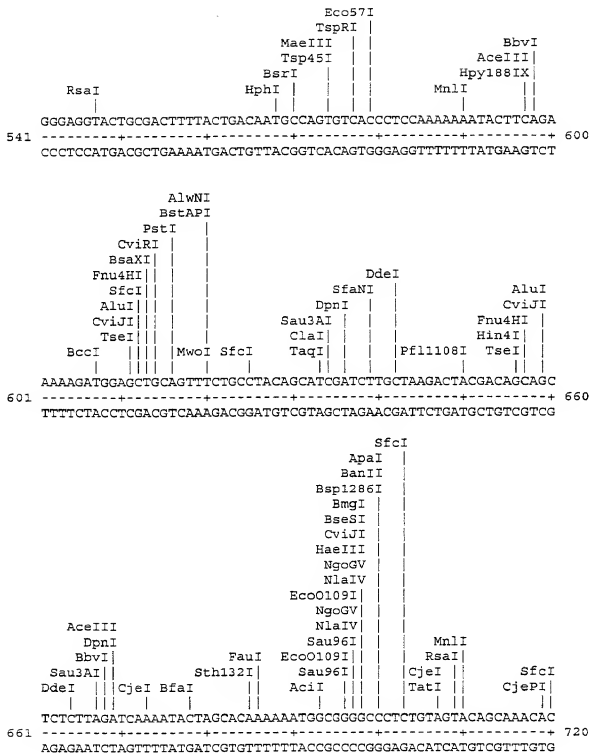






Figure 9 (continued)



Figure 9 (continued)

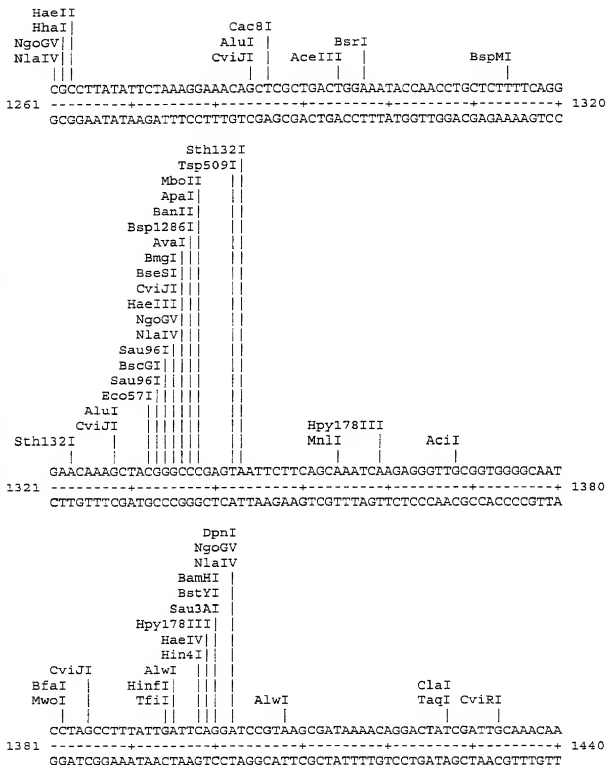
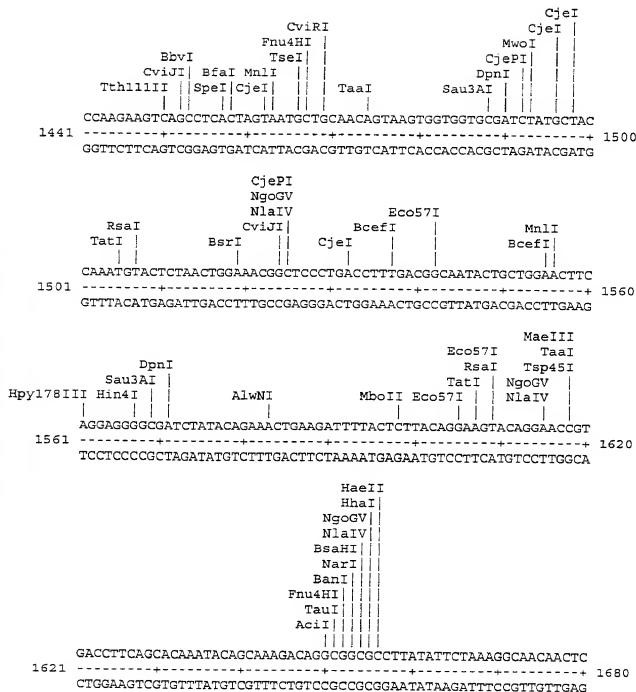


Figure 9 (continued)



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Figure 9 (continued)

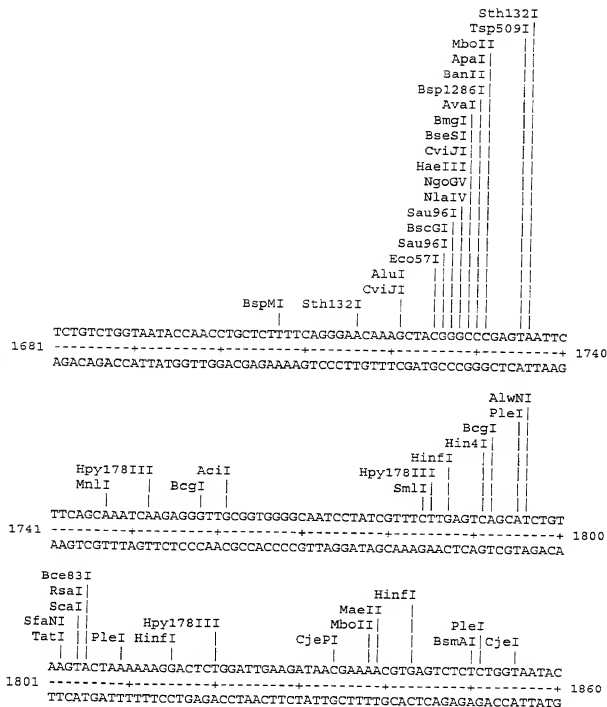
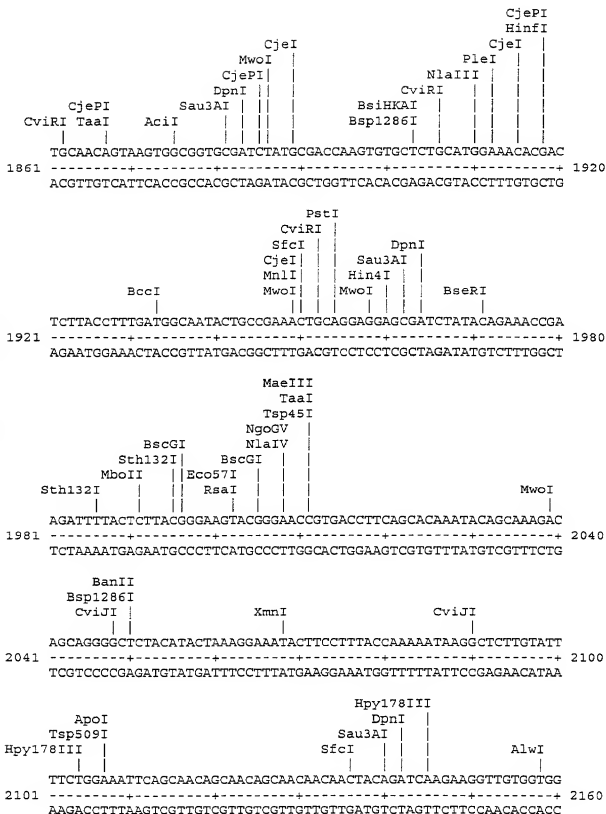


Figure 9 (continued)



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Figure 9 (continued)

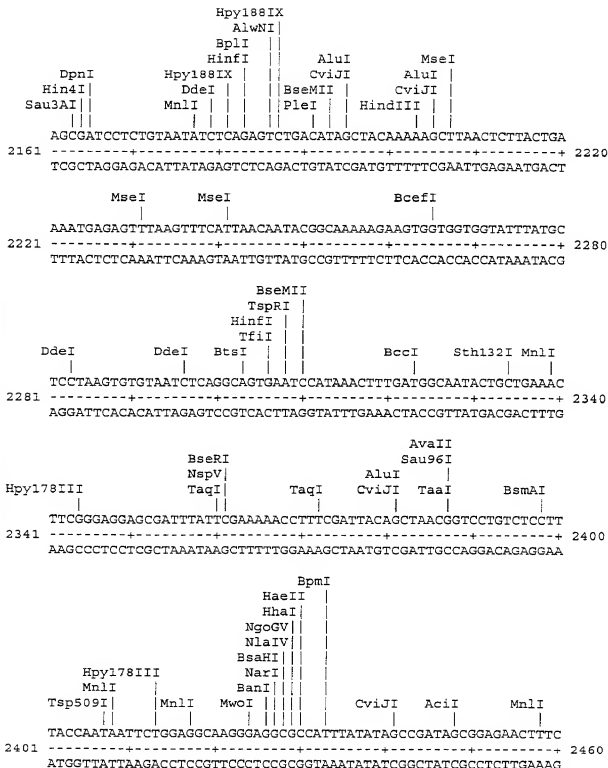




Figure 9 (continued)

	AvaII		BsmI		Hpy178III		
	Sau96I				SmlI		ApoI
	BsiI		Bce83I		CviJI		Tsp509I
	PflMI		MboII				
	AAATGGTCCTATATAGAGAAAAACGAATGCTCTTTGTAAGGCTCAAGAGTAAAAAATTC						
2701	-----+				-----+		2760
	TTTACCAGGATATATCTTCTTTTGCTTACGAGAAACATTCGGAGTTCCTCATTTTAAAG						
					Eco57I		
		Hpy188IX			ApoI		
		BceFI		Fnu4HI	EcoRI		
		BbvI		TseI	Tsp509I		
	TAAAGGTATTCTCTCAATAGGTTCTGAAGTGCTGCCGTAGAATTCATAAATATCTC						
2761	-----+				-----+		2816
	ATTTCATAAGAGAGTTATCCAAGACTTCACGACGGCATCTTAAGTATTTATAGAG						



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Figure 9

Restriction enzyme analysis of CPN100624 (RY 64 - SEQ ID NO. 9)

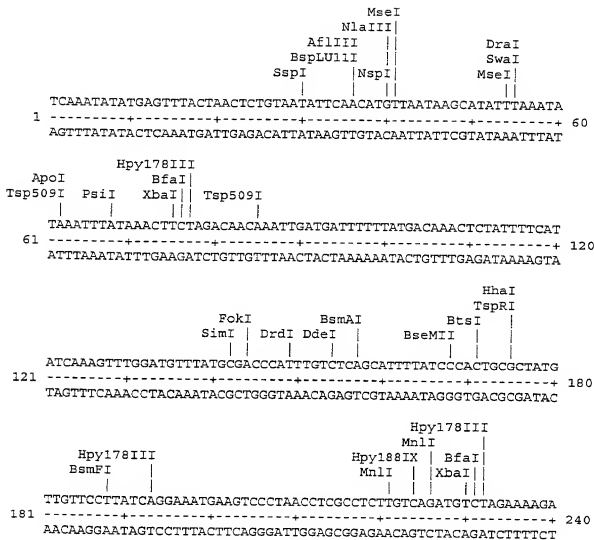
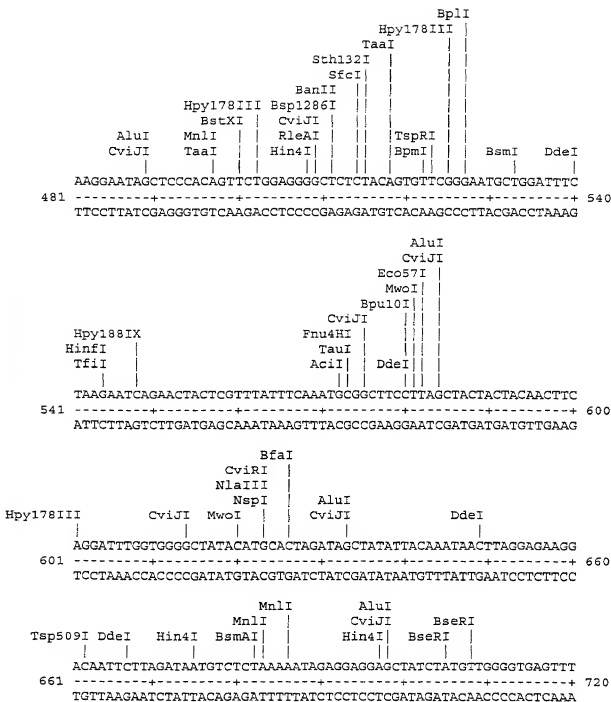


Figure 9 (continued)



Figure 9 (continued)





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Figure 9 (continued)

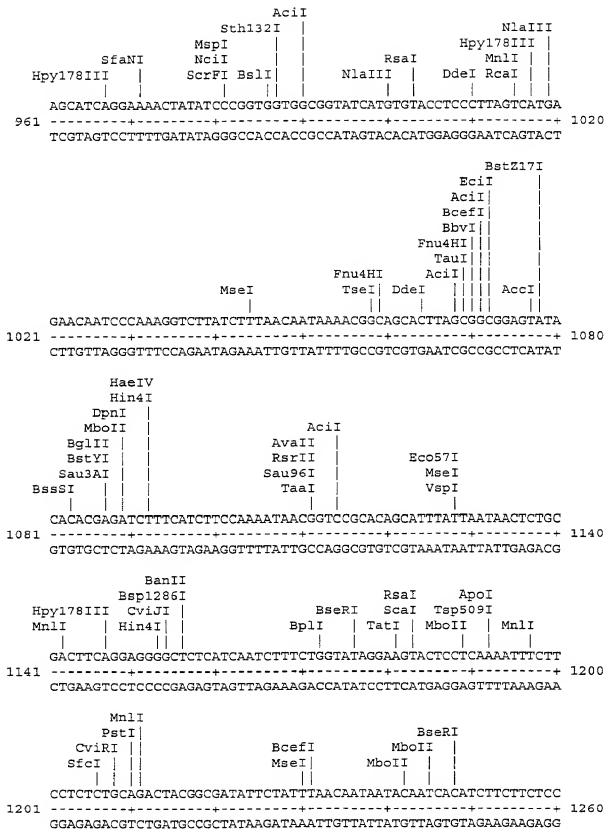
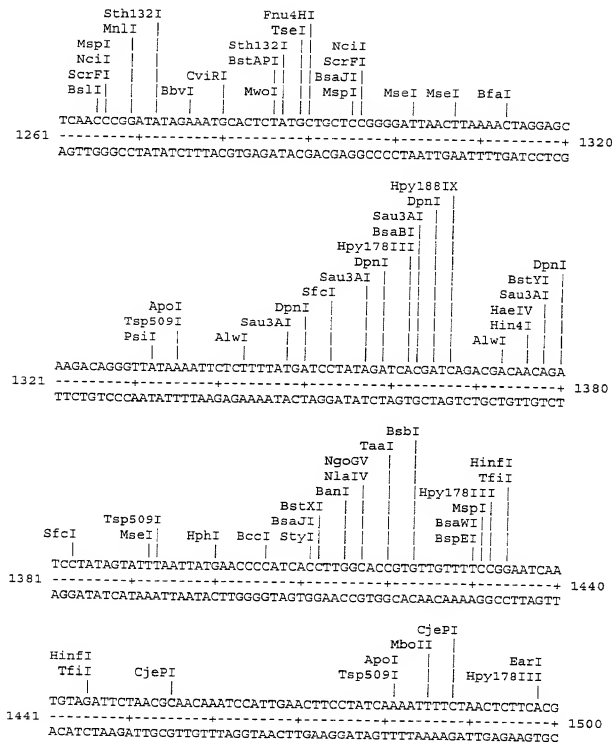


Figure 9 (continued)



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Figure 9 (continued)

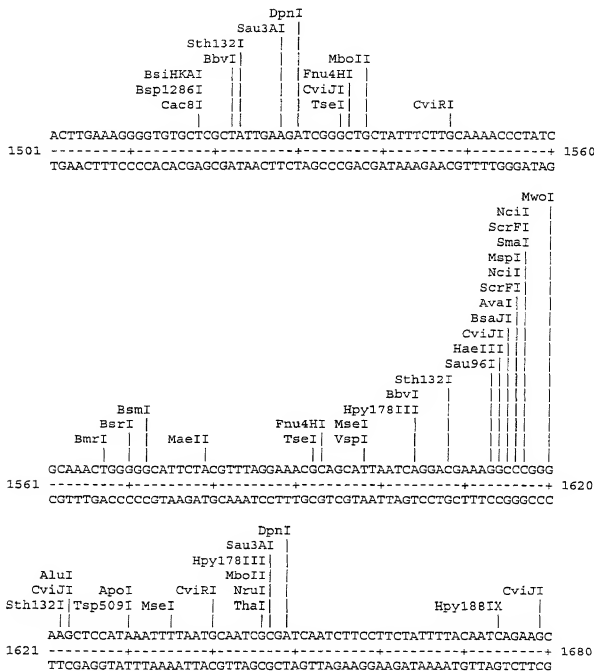


Figure 9 (continued)

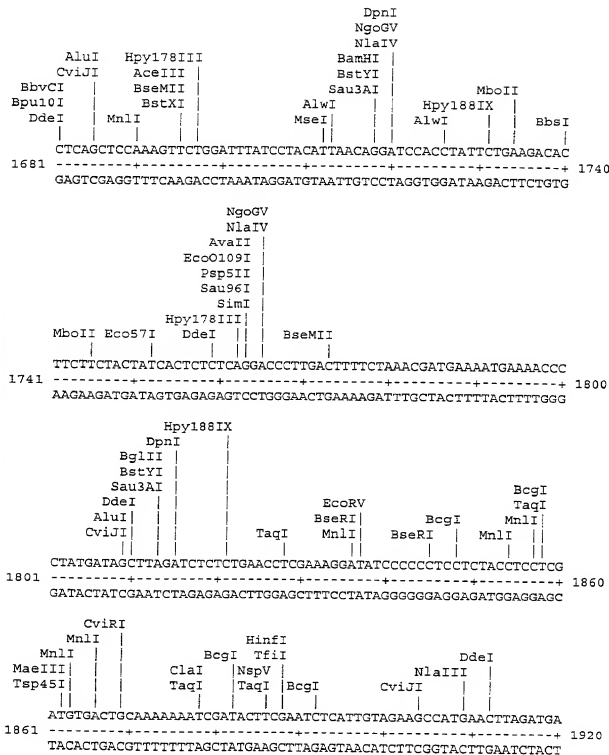




Figure 9 (continued)

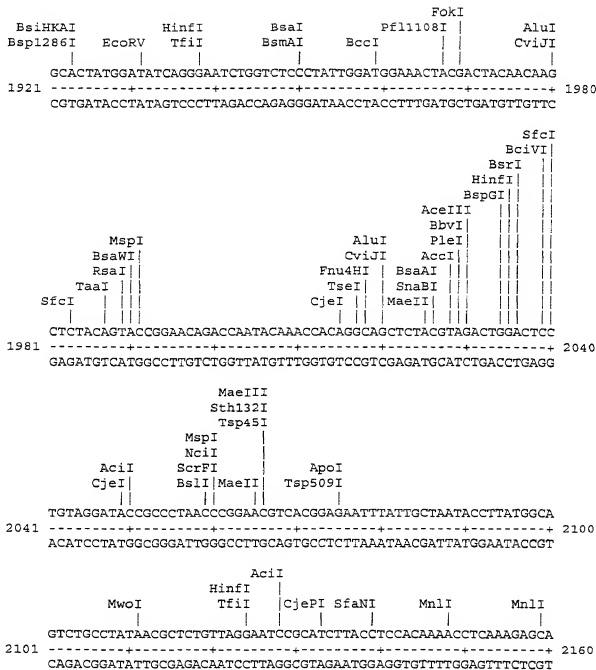


Figure 9 (continued)

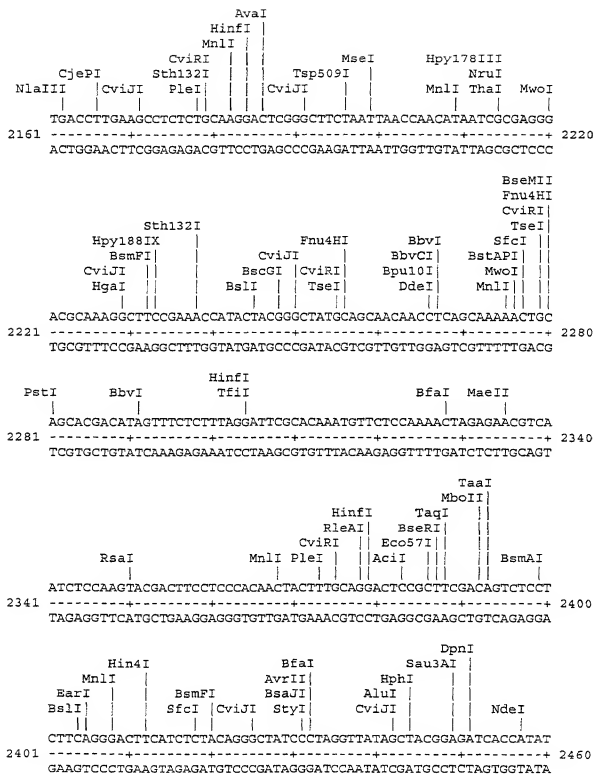
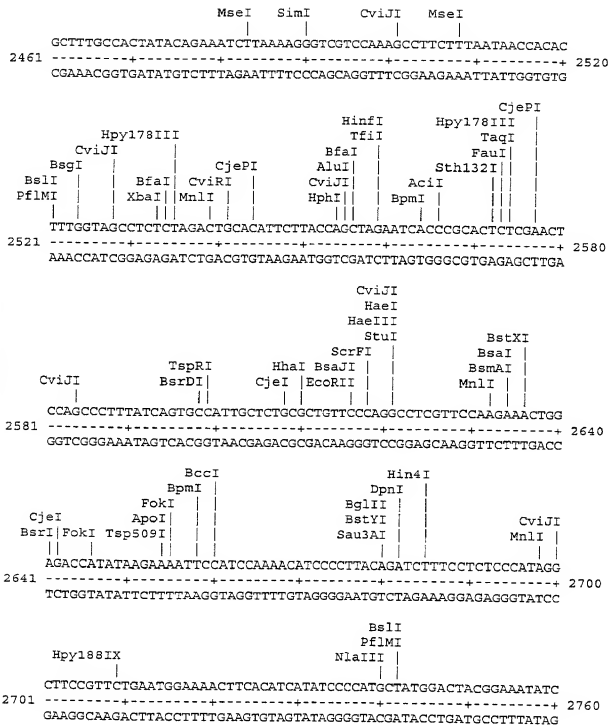


Figure 9 (continued)





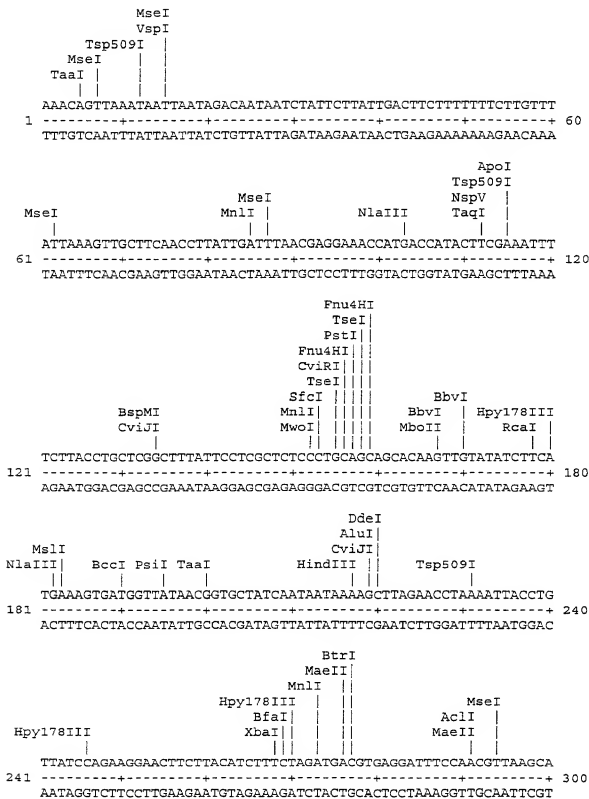
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Figure 9 (continued)

Tsp509I  
MseI  
CviJI  
NcoGV  
NlaIV  
TTGGAGCCTTAATTTTAGGTAAACTACAATA  
3061 -----+----- 3092  
AACCTCGGAATTAAATCCATTTTGATGTTAT

Figure 10

Restriction enzyme analysis of CPN100633 (RY 65 - SEQ ID NO. 10)



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Figure 10 (continued)

Hpy178III  
 DpnI  
 NlaIII  
 BclI  
 Sau3AI  
 SfaNI  
 DpnI  
 Sau3AI  
 ClaI  
 HinfI  
 TfiI  
 NlaIII  
 MmeI  
 MboII  
 PsiI  
 TaqI  
 301  
 TGATCAAGAAGATGCTGGGGTTTTTATAAATCGATCTGGGAATCTTTTTTCATGGGC  
 ACTAGTTCTTCTACGACCCCAAAAATATTAGCTAGACCCCTAGAAAAAAGTACCCGTT 360  
 CviRI  
 BstAPI  
 MwoI  
 TaaI  
 BbvI  
 BsaJI  
 MnlI  
 CjePI  
 Fnu4HI  
 HaeII  
 HhaI  
 TaqII  
 TseI  
 MmeI  
 NspV  
 TaqI  
 361  
 CCGTTGCAACTTCACTTTTACAACCTTATGACCGAGGGTTTGGCGCTGCCATTTCGAA  
 GGCACCTTGAAGTGAAAAGTGTGGAACTACTGGCTCCCAAAACCGCAGCGTAAAGCTT 420  
 CjePI  
 BsmAI  
 ThaI  
 AciI  
 CjePI  
 Tsp509I  
 CjePI  
 DdeI  
 HphI  
 Bce83I  
 BbvCI  
 Bpu10I  
 DdeI  
 421  
 CCGCGTTGGAGACACCACTCTCACTCTCTCTAATTTTTCTTACTTAGCGTTCACTCAGC  
 GCGCAACTCTCTGTGGTGAGAGTGAGAGAGATTAAAAAGAATGAATCGCAAGTGAGTGC 480  
 MnlI  
 SmlI  
 BseMII  
 MnlI  
 MnlI  
 HaeIV  
 HinfI  
 DrdII  
 NgoGV  
 NlaIV  
 DpnI  
 Sau3AI  
 MnlI  
 TaqI  
 481  
 ACCCTCTACTACCTCAAGGACAAGGAGCGATTATAGTCTTGTTCCGTGATGATCGAAAA  
 TGGAGATGATGGAGTTCTGTTCCTCGCTAAATATCAGAACCAAGGCCTACTAGCTTTT 540  
 MaeIII  
 RleAI  
 Tsp45I  
 Bsp24I  
 CjeI  
 CjePI  
 CjeI  
 MboII  
 CjeI  
 AceIII  
 CjeI  
 CjePI  
 Fnu4HI  
 AluI  
 Bsp24I  
 BbvI  
 TseI  
 CviJI  
 Hin4I  
 CjeI  
 541  
 TAGTGAGGAAGTGACTTTCTGTGGGAACCTACTCTTCTGTGGAGTGGAGCTGCGATTATAC  
 ATCACTCCCTCACTGAAAGACACCCTTGATGAGAGCACCTCACCTCGACGCTAAATATG 600

**CONCLUSIONS**



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Figure 10 (continued)

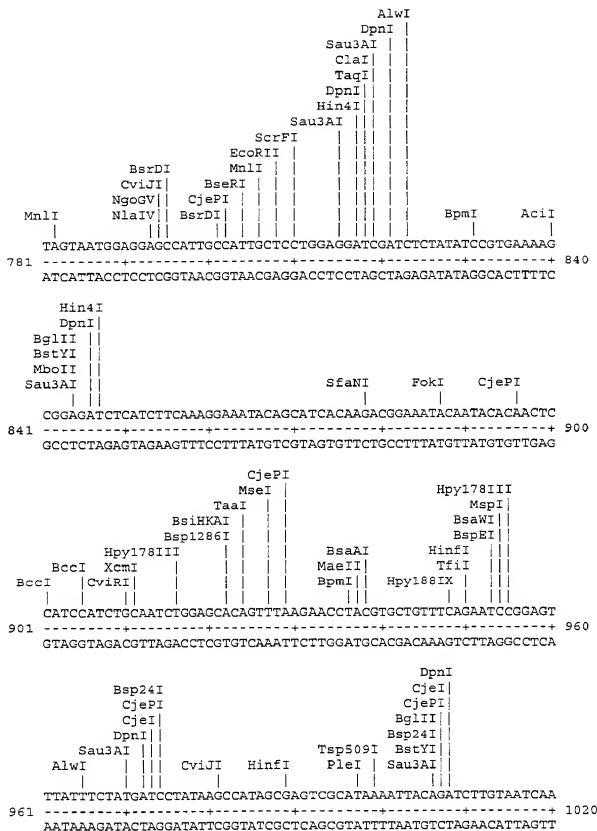


Figure 10 (continued)

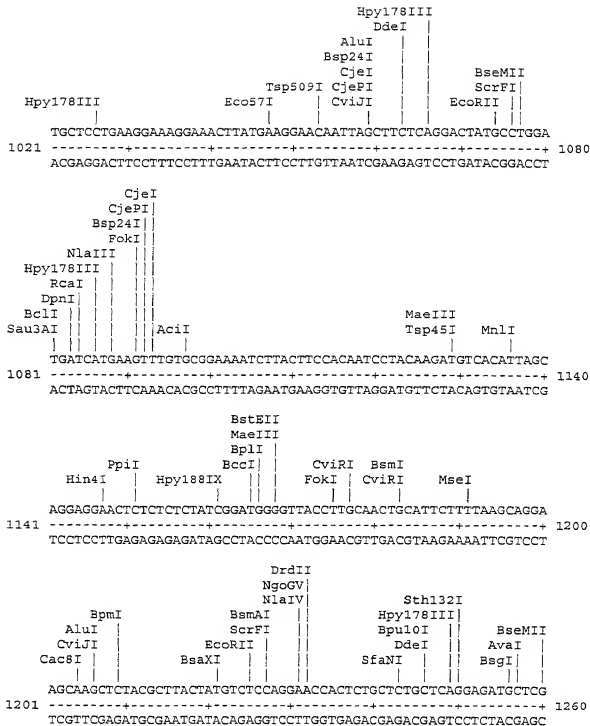


Figure 10 (continued)

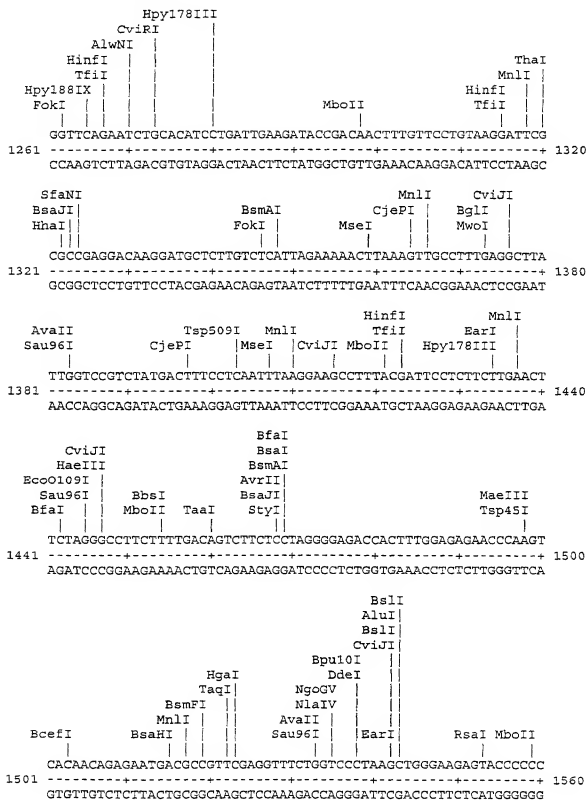


Figure 10 (continued)

[illegible]

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Figure 11

Restriction enzyme analysis of CPN100985 (RY 66 - SEQ ID NO. 11)

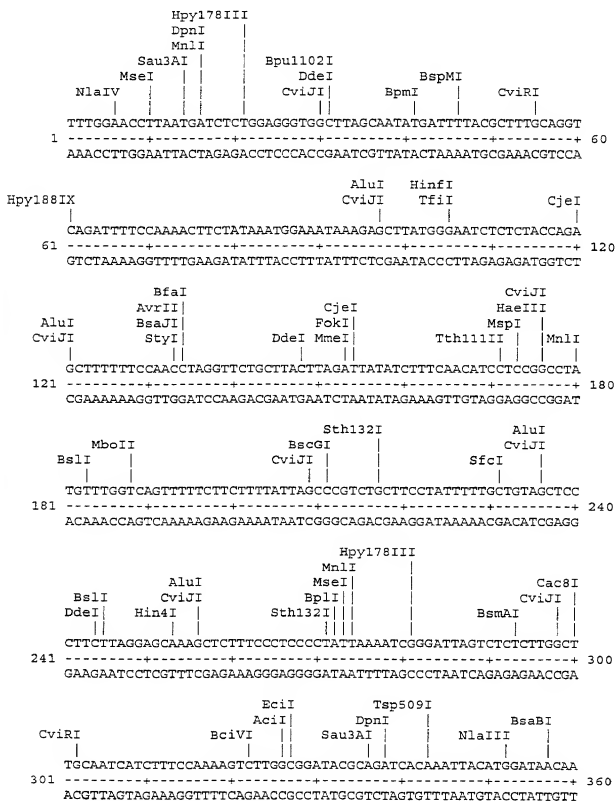
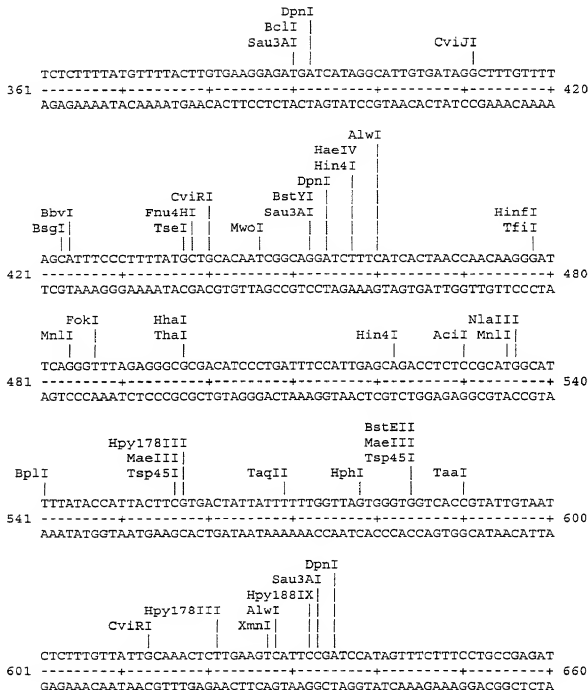


Figure 11 (continued)



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Figure 11 (continued)

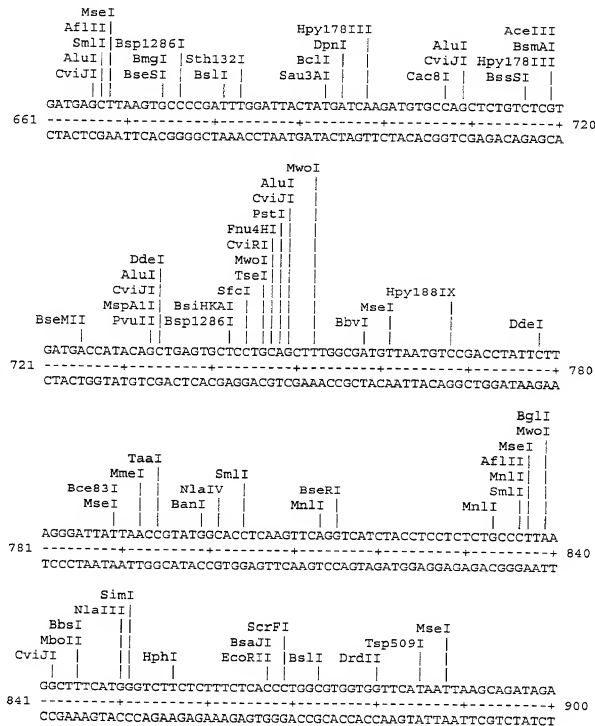
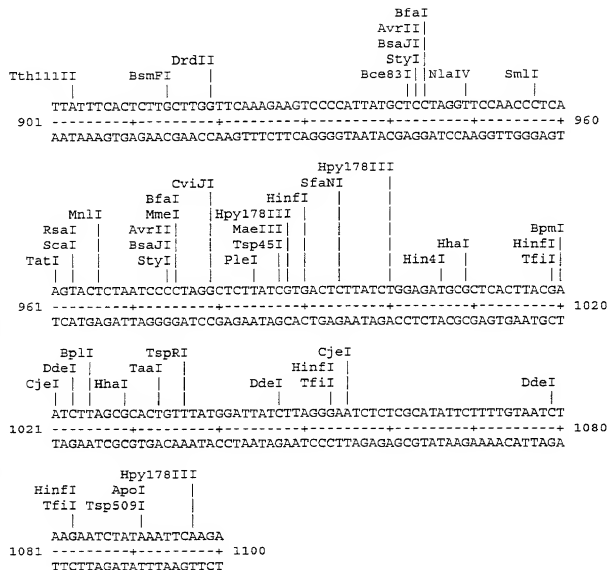


Figure 11 (continued)





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Figure 12

Restriction enzyme analysis of CPN100987 (RY 67 - SEQ ID NO. 12)

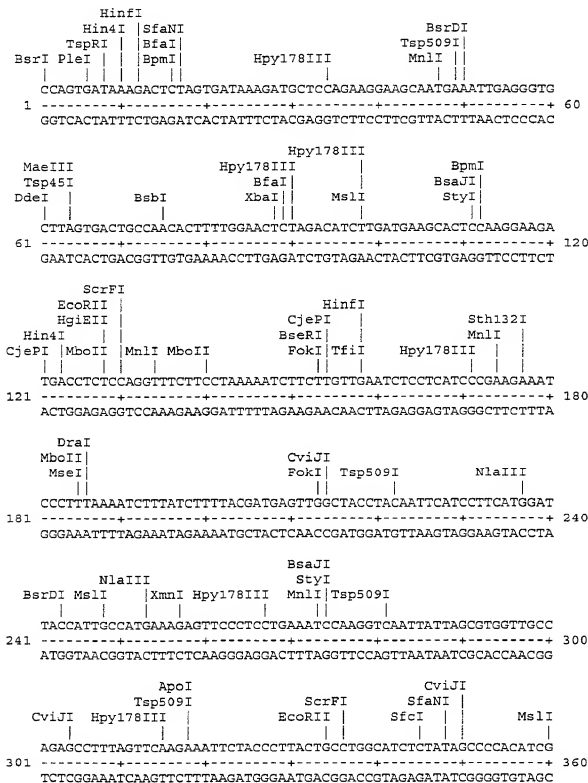
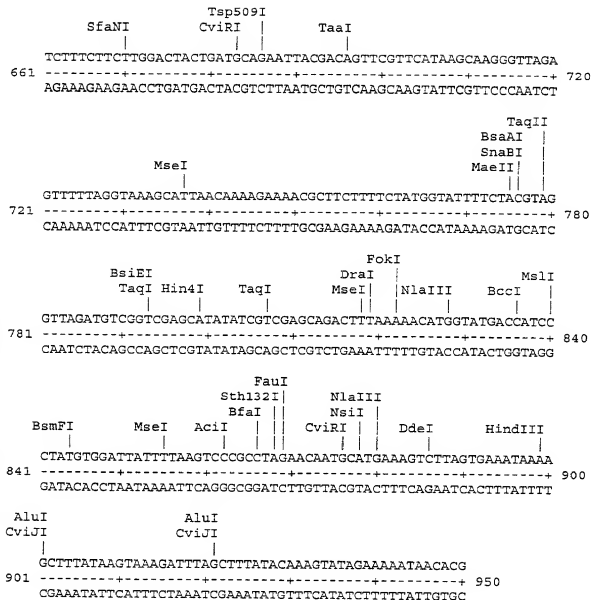




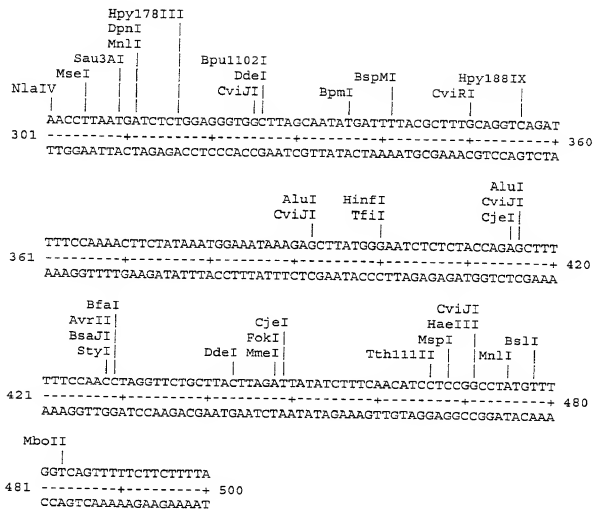
Figure 12 (continued)





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Figure 13 (continued)



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Figure 14: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 14; ORF: cpn100686

1 MVSSPILNVP LKNHASVSGK FTHREVSCLA SDLKSGAMSF VPEVLSEETI  
51 SSDLGKKQCT QGIISACGL AMLIVLMSVY YRFGGVIASG AVLLNLLLIW  
101 AALQYLDAPL TLISGLAGIVL AMGMAVDANV LVFERIREEF LLSQSLKKS  
151 EKGYTCAFGL IFDSNLTTVL ASALLFFLDT GPIKGFALTL ILGIFSSMPT  
201 ALFMTKFFFM LWMNKTQHTQ LHMMNKFVGI KHDFLRGCKK LWAVSGSVFL  
251 LGCVALGFGL WNSVLGMDFK GGYAFTFNPK EHGISDVAQM RGKVVKLQE  
301 AGLSSRDFFR QTFGSSEKIK IYFSDKALS YTKQIRASLLK LTIMSWRYCG  
351 IUVNRNPRFL YGNSKRNAKF WSKVSSKLSK KMRYQATIGL LGALAIILY  
401 VSLRFWEQYA FSAVCALIHDL LATCAVLFI AHFFLKKIQI DLQAIGALMT  
451 VLGYSLNNTL IIFDRIREDR QANLFTPMHV LVNDALQKTF SRTVMTTATT  
501 LSVLLMLLFI GGSSVFNFAP IMTIGILLGT LSSLYIAPPL LLFMVRKENR  
551 SK

Possible T cell epitope:

427 VLFIAHFFL

Possible B cell epitope:

465 RIREDRQAN

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Figure 15: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 15; ORF: cpn100696

1 MSSNLHPVGG TGTGAAAPES VLNIVEEIAA SGSVTAGLQA ITSSPGMVNL  
51 LIGWAKTKFI QPIRESKLFQ SRACQITLLV LGILLVVAGL ACMFIFHSQL  
101 GANAFWLIIP AAIGLIKLLV TSLCFDEACT SEKLMVFQKW AGVLEDQLDD  
151 GILNNSNKIF GHVKTEGNTS RATTPLNDG RGTPLVLSPLV SKIARV

Possible T cell epitope:

133 KLMVFQKWA

Possible B cell epitope:

163: VKTEGNTSRAT

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Figure 16: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 16; ORF: cpn100709

1 MTIRILAEGL AFRYGSKGFN IHDVSFSVY DGDFIGIIGP NGGKSTLTM  
51 LILGLLTPTF GSKTTPSHS AGKQTHSMIG WVPQHFSYDF CFPISVKDVV  
101 LSGRLSQLSW HGKYKKKDFE AVDHADLVG LSDTTTTTAF HLGGGQIQRV  
151 LLARALASYP EILILDEPTT NIDPDNQQR LSLKKNLRT CTILMVTHDL  
201 HHTTNYFNKV FYMNTLHFI GRHFDLNRPI LLSSYKNQEF SCSPH

Possible T cell epitope:

212 YMNKTLHFI

Possible B cell epitopes:

109 SWHGKYKKKDFE

166 DEPTTNIDPDNQQR



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Figure 17: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 17; ORF: cpn100710

1 MHKVIIVFIFL TLYSLKSYGN DVIDKPHVLV SIAPYKFLVE QIABETCFVY  
51 AIVTNHYDPH TYELPPQIQK ELRQGDWLFR IGEAFGKNLL EKPVMQQVDL  
101 SONVSLIQGK PCCNQHTTNY DHTWLSPKN LKVQVETIVT TLSKKYPOHA  
151 TLYQSNGEKL LLALDQLNEE ILTITSKAKQ RHILVSHGAF GYFCRDYNFS  
201 QHTIEKSSHV EPSPKDVARV FRDIEQYKIS SVILLEYSGR RSSAMLADRF  
251 HMHTVNLDPY AENVLVNLKT IATTFSSL

Possible T cell epitope:

125 WLSPKNLKV

Possible B cell epitope:

55 NHYDPHTYELPPQIQIKELRQGD

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**Figure 18:** Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 18; ORF: cpn100711

```

1  MGPGSVLSNH SKEAGGIAIN NVIIDFSEIV PTKDNATVAP PTLKLVSRTH
51 ADSKDKIDIT GTVTLLDPNG NLYQNSYLGE DRDITLFNID NSASGAVTAT
101 NVTLQGNLGA KKGYLGTWNL DPNSSGSKII LKWTFDKYLR WPIYIPRDNHF
151 YINSIWGAQN SLVTVNQGIL GNMLNNARFE DPAFNNFWAS AIGSFRLRKEV
201 SRNSDSFTYH GRGYTAAVDA KPRQEFILGA AFSQVFGHAE SEYHLDNYKH
251 KSGSGHSTQAS LYAGNIFYFP AIRSRPILFQ GVATYGYMQH DTTTYPSIE
301 EKNMANWDSI AWLFDLRFVS DLKEPQPHST ARLTFYTEAE YTRIRQEKFT
351 ELDYDPRSFS ACSYGNLAIP TGFSVDGALA WREIILYNKV SAAYLPVILR
401 NNPKATYEV LSTKEKGNVVN VLPTRNAARA EVSSQIYLG S YWTLYGTYTI
451 DASMNTLVQM ANGGIRFVF

```

Possible T cell epitope:

312 WLFDLRFVS

Possible B cell epitope:

240: ESEVHLDNYKHKGSGHST

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Figure 19: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 19; ORF: cpn100877

1 MRFSLCGFPL VFSFTLLSVF DTSLSATIS LTPEDSFHGD SQNAERSYNV  
 51 QAGDVYSLTG DVVISNVDNS ALNKACFNVT SGSVTFAGNH HGLYFNMISS  
 101 GTTKEGAVLC QQDPQATARF SGFSTLSPIQ SPGDIKEQGC LYSKALMLLL  
 151 NNYVVRFEQN QSKTKGGAIS GANVTIVGNY DSVSPYQNAF TFGGAHSSG  
 201 PLQIAVNAE IRFAQNTAKN GSGGALYSDG DIDIDQNAIV LFRENEALTT  
 251 AIGKGGAVCC LPTSGSSTPV PIVTFSDNKQ LVFERNHSHM GGGAIYARKL  
 301 SISSGGPTLF INNISYANSQ NLGGAIAIDT GGEISLSAEK GTITFQGNRT  
 351 SLPFLNGIHL LQNAKFLKLQ ARNGYSIEFY DPITSEADGS TQLNINGDPK  
 401 NKEYTGTILF SGEKSLANDP RDFKSTIPQN VNLSAGYLVI KEGAETVSK  
 451 FTQSPGSHLV LDLGKTLIAS KEDIAITGLA IDIDSLSSSS TAAVIKANTA  
 501 NKQISVTDISI ELISPTGNAY EDLRMRNSQT FPLLSLEPGA GGSVTVTAGD  
 551 FLFPVPHYGF QGNWKLAWTG TGNKVGEFFW DKINVKPRPE KEGNLVFNIL  
 601 WGNADVVRSL MQVQETHASS LQTDRLWID GIGNFFHVSA SEDNIRYRN  
 651 SGGYVLSVNN EITPKHYTSM AFSQLFSRDK DYAVSNMEYR MYLGSYLQY  
 701 TISLGNIFRY ASRNPVNVNG ILSRRFLQNP LMIFHFLCAY GHATNDMKTID  
 751 YANFPMVKNS WRNNCWAIEC GGSMPLLVFE NGRLFQGAIP FMKLQLVYAY  
 801 HGDFFKETTAD GRRFSNGSLT SISVPLGIRF EKLALSQDVL YDFSFSYIPD  
 851 IFRKDPSCBA ALVISGDSWL VPAAHVSRHA FVSGTGRYF FNDYTELLCR  
 901 GSIECRPHAR NYNINCGSKF RF

Possible T cell epitope:

146 ALMLLNMYV

Possible B cell epitope:

581 DKINVKPRPEKEG

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Figure 20: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 20; ORF: CPN100325

1 MPSSWKRLQ VLSHKIAATE SGGGIYAKDI QLQALPGSFT ITDNKVETSL  
51 TTSTNLYGGG IYSSGAVTLT NISGTFGITG NSVINTATSQ DADIQGGGIY  
101 ATTSLSINQC NTFILFSNNS AATKKTSTTK QIAGGAIFSA AVTIENNSQP  
151 IIFLNNSAKS EATTAATAGN KDSCGGAIAA NSVTLTNNPE ITFKGNVAET  
201 GGAIGCIDLT NGSPPRKVS I ADNGSVLFQD NSALNRGGAI YGETIDISRT  
251 GATFIGNSK HDGSAICCS T ALTLAPNSQL IPENNKVTET TATTKASINN  
301 LGAAIYGNN TSDVTISLSA ENGSIFKNN LCTATNKYCS IAGNVKFTAI  
351 EASAGKAISF YDAVNVPPKK QLLKS

Possible T cell epitope:

226 VLFQDNSAL

Possible B cell epitope:

257 NSSKHDG

91/96

Figure 21: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 21; ORF: CPN100368

1 MKYSLFWLLT SSALVFSLHP LMAANTDLSS SDNYENGSSG SAAFTAKETS  
 51 DASGTTTYTLT SDVSITNVSA ITPADKSCFT NTGGALS FVG ADHSLVLQTI  
 101 ALTHDGAALN NTWTALSFSG FSSLLIDSAP ATGTSOGKGA ICVTNTEGGT  
 151 ATFTDNASVT LQKNTSEKDG AAVSAYSIDL AKTTTAAALLD QNTSTKNGGA  
 201 LCSTANTTVQ GNSGTVTFSS NTATDKGGGI YSKEKDSTLD ANTGVVTFKS  
 251 NTAKTGGAWS SDDNLALTGN TQVLFQENKI TGSAAQANP ECGGGAICCY  
 301 LATATPKTGL AISQNQEMSF TSNITTANGG AIYATKCTLD GNTTLTFDQN  
 351 TATAGCGGAI YTETEDFSLK GSTGTVTFST NTAKTGGALY SKGNSSLTGN  
 401 TNLLFSGNKA TGPSNSSANQ ECGGGAIALF IDSGSVSDKT GLSIANNQEV  
 451 SLTSNAATVS GGAIYATKCT LTGNGSLTFD GNTAGTSGGA IYTETEDFTL  
 501 TGSTGTVTFSS TNTAKTGGAL YSKGNNSLSG NTNLLFSGNK ATGPSNSSAN  
 551 QEGCGGAILS FLESASVSTK KGLWIEDNEN VSLSGNTATV SGGAIYATKC  
 601 ALHGNTTLTF DGNTAETAGG AIYTETEDFT LTGSTGTVTF SNTAKTAGA  
 651 LHTKGNTSFT KSKALVFSGN SATATATTTT DQEGCGGAIL CNISESDIAT  
 701 KSLTLTENES LSPINNTAKR SGGGIYAPKC VISGESINF DGNTAETSGG  
 751 AIYSKNLSIT ANGPVSFTNN SGGKGGAIYI ADSGELSLEA IDGDITTFSGN  
 801 RATEGTSTPN SIHLGARGKI TKLAAAPGHT IYFYDPITME APASGGTIEE  
 851 LVINPVVKAI VPPPPQPKNGP I

Possible T cell epitope:

7 WLLTSSALV

Possible B cell epitopes:

162 QKNTSEKDG  
 538 GNKATGPSNSSANQEG

92/96

Figure 22: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 22; ORF: CPN100624

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1 MTNSIFISKF GCLCDPFVSA FYPTALCCSL SGNEVPNLAS CQMSRKDISA
51 FHTSPSFRNL VTPEPLVSSF RPSNLLNGFG HDITQDITIT GNSINSVIDY
101 NYHYEDGGIL ACKNLPISEN KGNLSFERNS SHSSGGALYS VRECWISKNQ
151 NYSFISNAAS LATTTTSGFG GAIHALDSYI TNNLGGGQFL DNVSKNRGGA
201 IYVGVSLSIT DNLGPIVIKK NQTLSDSSFG GGIFCRAVNI ERNYQNIQIN
251 DNASGQGQVYV FLPLGVISS NKEIIEISNH SASSINTASG KLYPGGGGIM
301 CTSLSHENNP KGLIFNNKTA ALSGGVYTRD LSSSKITVRT AFINNSATSG
351 GALINLSGIG STPQNFFLSA DYGDILFNNN TITSSSPQPG YRNALYAAPG
401 INLKLGARQG YKILFIDPID HDQTTTDPIV FNYEPHHLGT VLFSGINVDS
451 NATNPLNPLS KFSNSSRLER GVLAIEDRAA ISCKTLSQTG GILRLGNAAL
501 IRTKGPSSSI NFNAIAINLP SILQSEASAP KFWIYPTLTG STYSEDTSST
551 IITLGGPLTFL NDENENPYDS LDLSEPRKDI PPPLPPRCDC KKIDTSNLIV
601 EAMNLDEHYG YQGIWSPYWM ETTTTTSTV PEQNTNTHRQ LYVDWTPVGV
651 RPNPERHGEF IANTLWQAY NALLGIRILP PQNLKEHDLE ASLQGLGLLI
701 NQHNREGKRG FRNHTTGYAA TTSAKTAARH SPSLGFQMF SKTRERQSPS
751 TTSSHNYFAG LRFDSLFRD FISTGLSLGY SYGDHMLCH YTEILKGSSK
801 AFFNNHTLVA SLDCTFLPAR ITRTLELQPF ISAIALRCSQ ASFQETGDHI
851 RKFPKHPKPLT DLSSPIGERS EWKTSHHIPM LWTTEISYVP TLYRKNPEMF
901 TTLISNGTW TTQATPVSYN SVAAKIKNTS QLFSRVTLSL DYSAQVSSST
951 VQQLKKAESH CTF

```

Possible T cell epitope:

640 QLYVDWTPV

Possible B cell epitopes:

701 NQHNREGKRGFRNHTTG

741 SKTRERQSPSTSSHNY

93/96

Figure 23: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 23; ORF: CPN100633

```

1 MTILRNFLTC SALFLALPAA AQVVYLHESD GYNGAINNKS LEPKITYPE
51 GTSYIFLDDV RISNVKHDQE DAGVFINRSG NLFFMGNRNCF FTFPHLMTEG
101 FGAAISNRVG DTTLTLSNFS YLAFTSAPLL PQQGGAIIYSL GSVMIENSEE
151 VTFCGNYSSW SGAAIYTPYL LGSKASRPSV NLSGNRYLVF RDNVSVQVYGG
201 AISTHNLTLT TRGPSCFENN HAYHDVNSNG GAIAIAPGGS ISISVKSGDL
251 IFKGNITASQD GNTIHNHSL QSGAQFKNLR AVSESGVYFY DPIHSHESHK
301 ITDLVINAPE GKETYEGTIS FSGLCDDHE VCAENLTSTI LQDVTLAGGT
351 LSLSDGVTLQ LHSFKQEASS TLTMSPGTTL LCSGDARVON LHILIEDTDN
401 FVPVRIRAEK KDALVSLKEL KVAPEAYWSV YDFPQFKEAF TIPLLELLGP
451 SFDLLLLGET TLERTQVTE NDAVRGFWSL SWEEYPPSLD KDRRITPTKK
501 TVFLTWNPEI TSTP

```

Possible T cell epitope:

640 QLYVDWTPV

Possible B cell epitope:

482 WEEYPPSLDKDRRITPTKK

94/96

Figure 24: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 24; ORF: cpn100985

1 MGISLPELFS NLGSAYLDYI FQHPPAYVWS VFLLLLARLL PIFAVAPFLG  
51 AKLFPSPIKI GISLSWLAI FPKVLADTQI TNYMDNNLFY VLLVKEMIIG  
101 IVIGFVLAFP FYAAQSAGSF ITNQOGIQGL EGATSLISIE QTSPhGILYH  
151 YFVTIIFWL V GGHRIVISLL LQTELEVIPIH SFFPAENMSL SAPIWITMIK  
201 MCQLCLVMTI QLSAPAALAM LMSDLFLGII NRMAPOVQVI YLLSALKAFM  
251 GLLFLTAWW FIIKQIDYFT LAWFKEVPIM LLGSNPQVL

Possible T cell epitope:

83 YMDNNLFYV

Possible B cell epitope:

78 TQITNYMDNN



95/96

Figure 25: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 25; ORF: cpl00987

```
1 MKHSKEDDLRS RFLPKNLLVE SPHPSEIPLK SLSFTMSWLP TIHPSWITIA
51 MKEFPPEIQG QLLAWLPEPL VQEILPLLPG ISIAPHRCAP FGAFYLLDML
101 SKKIRPCGIT EEIFLPASSA NAILYYTGPV KIALINCLGL YSIAKELKHI
151 LDKVVIKRVK NALSPTKELF LTYCQSHPMK HLETTNPLSS WTTDAELROF
201 VHKQGLEFLG KALTKENASF LWYFLRRLDV GRAYIVEQTL KTWYDHPYVD
251 YFKSRLEQCM KVLVK
```

Possible T cell epitope:

220 FLWYFLRRL

Possible B cell epitope:

1 MKHSKEDDLRS

96/96

Figure 26: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 26; ORF: cpn100988

1 MLAFFATSPK SVLFEYSYQS LLLILIVSAP PIILASIVGI MVAIFQAATQ  
51 IQEQTFAPAV KLVVIFGTLM ISGGWLSNMI LRFAGQIFQN FYKWK

Possible T cell epitope:

21 LLLILIVSA

Possible B cell epitope:

89 QNFYKWK

77813-73/ccm

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

## COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; that I verily believe that I am the original, first and sole inventor (if only one name is listed below) or a joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF**

the specification of which

- ☐ is attached hereto.
- ☒ was filed on June 21, 2001  
as U.S. Application Serial No. 09/868,987
- ☒ was filed on December 23, 1999  
as PCT International Application No. PCT/CA99/01230

and (if applicable) was amended on February 13, 2001

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information known to me which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §§1.56(a) and (b), which state:

- "(a) A patent by its very nature is affected with a public interest. The public interest is best served, and the most effective patent examination occurs when, at the time an application is being examined, the Office is aware of and evaluates the teachings of all information material to patentability. Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose information exists with respect to each pending claim until the claim is cancelled or withdrawn from consideration, or the application becomes abandoned. Information material to the patentability that is cancelled or withdrawn from consideration need not be submitted if the information is not material to the patentability of any claim remaining under consideration in the application. There is no duty to submit information which is not material to the patentability of any existing claim. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§1.97(b)-(d) and 1.98. However, no patent will be granted on an application in connection with which fraud on the Office was practiced or attempted or the duty of disclosure was violated through bad faith or intentional misconduct. The Office encourages applicants to carefully examine:
- (1) prior art cited in search reports of a foreign patent office in a counterpart application,
  - (2) the closest information over which individuals associated with the filing or prosecution of a patent application believe any pending claim patentably defines, to make sure that any material information contained therein is disclosed to the Office.

- 2 -

- (b) Under this section, information is material to patentability when it is not cumulative to information already of record or being made of record in the application, and
- (1) It establishes, by itself or in combination with other information, a prima facie case of unpatentability of a claim; or
  - (2) It refutes, or is inconsistent with, a position the applicant takes in:
    - (i) Opposing an argument of unpatentability relied on by the Office, or
    - (ii) Asserting an argument of patentability.

A prima facie case of unpatentability is established when the information compels a conclusion that a claim is unpatentable under the preponderance of evidence, burden-of-proof standard, giving each term in the claim its broadest reasonable construction consistent with the specification, and before any consideration is given to evidence which may be submitted in an attempt to establish a contrary conclusion of patentability."

I hereby claim foreign priority benefits under 35 United States Code, §119 and/or §365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate filed by me or my assignee disclosing the subject matter claimed in this application and having a filing date (1) before that of the application on which priority is claimed, or (2) if no priority claimed, before the filing of this application:

PRIOR FOREIGN APPLICATION(S)

<u>Number</u>	<u>Country</u>	<u>Filing Date</u> <i>(Day/Month/Year)</i>	<u>Date First</u> <u>Laid-open or</u> <u>Published</u>	<u>Date Patented</u> <u>or Granted</u>	<u>Priority</u> <u>Claimed?</u>
---------------	----------------	---	--	---	------------------------------------

I hereby claim the benefit under 35 United States Code, §119(e) of any United States provisional application(s) listed below:

<u>Application Number</u>	<u>Filing Date</u>
60/113,280	December 23, 1998
60/113,281	December 23, 1998
60/113,282	December 23, 1998
60/113,283	December 23, 1998
60/113,284	December 23, 1998
60/113,285	December 23, 1998
60/113,385	December 23, 1998
60/114,050	December 28, 1998
60/114,056	December 28, 1998
60/114,057	December 28, 1998
60/114,058	December 28, 1998
60/114,059	December 28, 1998
60/114,061	December 28, 1998

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is material to patentability as defined in

- 3 -

Title 37, Code of Federal Regulations, §1.56(a) which became available between the filing date of the prior application and the national or PCT international filing date of this application:

PRIOR U.S. OR PCT APPLICATION(S)

<u>Application No.</u>	<u>Filing Date</u> (day/month/year)	<u>Status</u> (pending, abandoned, granted)
------------------------	--	--

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

I hereby appoint the following patent agents with full power of substitution, association and revocation to prosecute this application and/or international application and to transact all business in the Patent and Trademark Office connected therewith:

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09-27-81 09:42

-4-

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## SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

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	Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp His His Met Leu Cys	
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 Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser Ala Ile Ala Leu Arg  
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tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc 2659  
 Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe  
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cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt 2707  
 His Pro Lys His Pro Leu Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg  
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	Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln			
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	Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met			
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	ggc gct gcc att tgc aac cgc gtt gga gac acc act ctc act ctc tct	451		
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	Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile			
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40	tat act ccc tac ctt tta ggt tct aag gcg agt cgt cct tca gta aat	643		
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	Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Thr Ala Ser Gln Asp Gly	250 255 260
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	aac cta cgt gct gtt tca gaa tcc gga gtt tat ttc tat gat cct ata	979
	Asn Leu Arg Ala Val Ser Glu Ser Ser Gly Val Tyr Phe Tyr Asp Pro Ile	280 285 290
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	Ser His Ser Glu Ser His Lys Ile Thr Asp Leu Val Ile Asn Ala Pro	295 300
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	Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys	310 315 320 325
	ctg gat gat cat gaa gtt tgt gcg gaa aat ctt act tcc aca atc cta	1123
	Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu	330 335 340
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 Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu  
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 Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro  
 150 155 160 165

	aca gag aaa c c ttt ctt acc tac tgc caa tct cat ccg atg aaa cat	643
	Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His	
	170 175 180	
	tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta	691
	Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu	
	185 190 195	
10	cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta	739
	Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu	
	200 205 210	
	aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat	787
	Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp	
	215 220 225	
	gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac	835
	Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp	
	230 235 240 245	
20	cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa	883
	His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys	
	250 255 260	
	gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta	935
	Val Leu Val Lys	
	265	
30	tagaaaaata acacg	950
	<210> 13	
	<211> 500	
	<212> DNA	
	<213> Chlamydia pneumoniae	
	<220>	
	<221> CDS	
	<222> (101) .. (385)	
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	cgatttcggtt accttttaaag ttacttttga tcgtcatggt agacggatgg acattactgc 60	
	tccaagggctt tatgatcagc tttaaataag gacacgtgcc atg tta gca ttt ttc	115
	Met Leu Ala Phe Phe	
	1 5	
	gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta	163
	Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu	
	10 15 20	
50	tta ctt att ttg att gtt tcg gca cct ccc atc atc tta gct tcc ata	211
	Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile	
	25 30 35	
	gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa	259
	Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu	
	40 45 50	

cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta 307  
 Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu  
 55 60 65

atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt 355  
 Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly  
 70 75 80 85

10 cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct 405  
 Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
 90 95

ctctaccaga gctttttttcc aacctaggtt ctgcttactt agattatatc ttccaacatc 465  
 ctccggccta tggttggtca gttttttcttc tttta 500

20 <210> 14  
 <211> 552  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 14  
 Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser  
 1 5 10 15  
 Val Ser Gly Lys Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp  
 20 25 30  
 30 Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu  
 35 40 45  
 Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile  
 50 55 60  
 Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr  
 65 70 75 80  
 Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu  
 85 90 95  
 40 Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu  
 100 105 110  
 Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala  
 115 120 125  
 Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln  
 130 135 140

50 Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala  
 145 150 155 160  
 Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe  
 165 170 175  
 Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu  
 180 185 190

Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe  
 195 200 205  
 Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met  
 210 215 220  
 Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys  
 225 230 235 240  
 10 Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu  
 245 250 255  
 Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly  
 260 265 270  
 Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala  
 275 280  
 20 Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser  
 290 295 300  
 Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys  
 305 310 315 320  
 Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala  
 325 330 335  
 30 Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val  
 340 345 350  
 Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala  
 355 360 365  
 Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr  
 370 375 380  
 Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr  
 385 390 395 400  
 40 Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala  
 405 410 415  
 Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His  
 420 425 430  
 Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu  
 435 440 445  
 50 Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp  
 450 455 460  
 Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val  
 465 470 475 480  
 Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr  
 485 490 495



Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly  
 500 505 510  
 Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu  
 515 520 525  
 Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met  
 530 535 540  
 10 Val Arg Lys Glu Asn Arg Ser Lys  
 545 550  
 <210> 15  
 <211> 196  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 15  
 20 Met Ser Ser Asn Leu His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala  
 1 5 10 15  
 Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly  
 20 25 30  
 Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val  
 35 40 45  
 30 Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg  
 50 55 60  
 Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val  
 65 70 75 80  
 Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe  
 85 90 95  
 His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala  
 100 105 110  
 40 Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala  
 115 120 125  
 Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu  
 130 135 140  
 Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe  
 145 150 155 160  
 50 Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val  
 165 170 175  
 Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys  
 180 185 190  
 Ile Ala Arg Val  
 195

<400> 16  
Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser  
1 5 10 15

Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu  
35 40 45

Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly  
20 65 70 75 80

Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly  
100 105 110

30 Val Gly Leu Ser Asp Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly  
130 135 140

Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn  
165 170 175

Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn  
195 200 205

50 Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe  
225 230 235 240

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<210> 17
<211> 278
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&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 17

Met His Lys Val Ile Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys  
 1 5 10 15

Ser Tyr Gly Asn Asp Val Ile Asp Lys Pro His Val Leu Val Ser Ile  
 20 25 30

10

Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe  
 35 40 45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu  
 50 55 60

Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg  
 65 70 75 80

20

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln  
 85 90 95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys  
 100 105 110

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro  
 115 120 125

30

Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys  
 130 135 140

Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu  
 145 150 155 160

Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser  
 165 170 175

Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr  
 180 185 190

40

Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser  
 195 200 205

His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile  
 210 215 220

Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg  
 225 230 235 240

50

Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn  
 245 250 255

Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala  
 260 265 270

Thr Thr Phe Ser Ser Leu  
 275

<210> 18  
 <211> 469  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 18

Met Gly Pro Gly Ser Val Leu Ser Asn His Ser Lys Glu Ala Gly Gly  
 1 5 10 15

10 Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val Pro Thr  
 20 25 30

Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg  
 35 40 45

Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr  
 50 55 60

20 Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu  
 65 70 75 80

Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala  
 85 90 95

Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys  
 100 105 110

30 Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys  
 115 120 125

Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile  
 130 135 140

Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn  
 145 150 155 160

Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn  
 165 170 175

40 Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile  
 180 185 190

Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr  
 195 200 205

Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln  
 210 215 220

50 Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu  
 225 230 235 240

Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser  
 245 250 255

Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile  
 260 265 270

Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met  
275 280 285

Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met  
290 295 300

Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val  
305 310 315 320

10 Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr  
325 330 335

Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu  
340 345 350

Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala  
355 360 365

20 Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile  
370 375 380

Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg  
385 390 395 400

Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly  
405 410 415

30 Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val  
420 425 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr  
435 440 445

Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly  
450 455 460

Ile Arg Phe Val Phe  
465

40

&lt;210&gt; 19

&lt;211&gt; 922

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 19

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu  
1 5 10 15

50 Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr  
20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr  
35 40 45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile  
50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr  
 65 70 75 80  
 Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn  
 85 90 95  
 Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln  
 100 105 110  
 10 Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe  
 115 120 125  
 Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys  
 130 135 140  
 Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn  
 145 150 155 160  
 20 Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile  
 165 170 175  
 Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe  
 180 185 190  
 Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln  
 195 200 205  
 30 Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly  
 210 215 220  
 Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val  
 225 230 235 240  
 Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly  
 245 250 255  
 Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile  
 260 265 270  
 40 Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser  
 275 280 285  
 Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser  
 290 295 300  
 Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln  
 305 310 315 320  
 50 Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu  
 325 330 335  
 Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu  
 340 345 350  
 Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys  
 355 360 365

Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr  
 370 375 380  
 Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys  
 385 390 395 400  
 Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu  
 405 410 415  
 10 Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn  
 420 425 430  
 Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val  
 435 440 445  
 Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly  
 450 455 460  
 20 Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala  
 465 470 475 480  
 Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys  
 485 490 495  
 Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu  
 500 505 510  
 Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser  
 515 520 525  
 30 Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val  
 530 535 540  
 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe  
 545 550 555 560  
 Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly  
 565 570 575  
 40 Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu  
 580 585 590  
 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg  
 595 600 605  
 Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp  
 610 615 620  
 Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala  
 625 630 635 640  
 50 Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu  
 645 650 655  
 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe  
 660 665 670

Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu  
 675 680 685  
 Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu  
 690 695 700  
 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly  
 705 710 715 720  
 10 Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe  
 725 730 735  
 Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala  
 740 745 750  
 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile  
 755 760 765  
 20 Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu  
 770 775 780  
 Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr  
 785 790 795 800  
 His Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn  
 805 810 815  
 Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys  
 820 825 830  
 30 Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile  
 835 840 845  
 Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile  
 850 855 860  
 Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala  
 865 870 875 880  
 40 Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu  
 885 890 895  
 Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr  
 900 905 910  
 Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe  
 915 920  
 50 <210> 20  
 <211> 375  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 20  
 Met Pro Ser Ser Trp Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile  
 1 5 10 15



Ala Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu  
20 25 30

Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr  
35 40 45

Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser  
50 55 60

10 Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly  
65 70 75 80

Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly  
85 90 95

Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr  
100 105 110

20 Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr  
115 120 125

Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile  
130 135 140

Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser  
145 150 155 160

Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly  
165 170 175

30 Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr  
180 185 190

Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp  
195 200 205

Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly  
210 215 220

40 Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile  
225 230 235 240

Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly  
245 250 255

Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu  
260 265 270

50 Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr  
275 280 285

Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala  
290 295 300

Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala  
305 310 315 320

Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn  
325 330 335

Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala  
340 345 350

Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro  
355 360 365

10    Lys   Lys   Gln   Leu   Leu   Lys   Ser  
               370                                  375

<210> 21

<211> 871

<212> PRT

<213> Chlamydia pneumoniae

20 Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe  
1 5 10 15

Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp  
20 25 30

Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu  
35 40 45

30 Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser  
50 55 60

Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr  
65 70 75 80

Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val  
85 90 95

Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr  
100 105 110

Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser  
115 120 125

Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr  
130 135 140

Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr  
145 150 155 160

50    Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr  
                    165                    170                    175

Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn  
180 185 190

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr  
195 200 205

Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr  
210 215 220

Asp Lys Gly Gly Gly Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp  
225 230 235 240

Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly  
245 250 255

10 Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln  
260 265 270

Val Leu Phe Gln Glu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn  
275 280 285

Asn Pro Glu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala  
290 295 300

Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe  
305 310 315 320

Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys  
325 330 335

Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala  
340 345 350

Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser  
355 360 365

30 Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys  
370 375 380

Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn  
385 390 395 400

Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser  
405 410 415

40 Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp  
420 425 430

Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln  
435 440 445

Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile  
450 455 460

Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp  
465 470 475 480

50 Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu  
485 490 495

Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn  
500 505 510

Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu  
 515 520 525  
 Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro  
 530 535 540  
 Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser  
 545 550 555  
 10 Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu  
 565 570 575  
 Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly  
 580 585 590  
 Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu  
 595 600 605  
 20 Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr  
 610 615 620  
 Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe  
 625 630 635 640  
 Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn  
 645 650 655  
 30 Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala  
 660 665 670  
 Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala  
 675 680 685  
 Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr  
 690 695 700  
 Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg  
 705 710 715 720  
 40 Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu  
 725 730 735  
 Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile  
 740 745 750  
 Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr  
 755 760 765  
 50 Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly  
 770 775 780  
 Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn  
 785 790 795 800  
 Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala  
 805 810 815

Val Ser Lys Asn Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser  
195 200 205

Ile Thr Asp Asn Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu  
 210 215 220  
 Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile  
 225 230 235 240  
 Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln  
 245 250 255  
 10 Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys  
 260 265 270  
 Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala  
 275 280 285  
 Ser Gly Lys Leu Tyr Pro Gly Gly Gly Ile Met Cys Thr Ser Leu  
 290 295 300  
 20 Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala  
 305 310 315 320  
 Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile  
 325 330 335  
 Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala  
 340 345 350  
 30 Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu  
 355 360 365  
 Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser  
 370 375 380  
 Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly  
 385 390 395 400  
 Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr  
 405 410 415  
 40 Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn  
 420 425 430  
 Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val  
 435 440 445  
 Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn  
 450 455 460  
 50 Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala  
 465 470 475 480  
 Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly  
 485 490 495  
 Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe  
 500 505 510

Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser  
 515 520 525  
 Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser  
 530 535 540  
 Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu  
 545 550 555 560  
 10 Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro  
 565 570 575  
 Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys  
 580 585 590  
 Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His  
 595 600 605  
 20 Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr  
 610 615 620  
 Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln  
 625 630 635 640  
 Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg  
 645 650 655  
 His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala  
 660 665 670  
 30 Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp  
 675 680 685  
 Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Ile Asn Gln His Asn  
 690 695 700  
 Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala  
 705 710 715 720  
 40 Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe  
 725 730 735  
 Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr  
 740 745 750  
 Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe  
 755 760 765  
 50 Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp  
 770 775 780  
 His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys  
 785 790 795 800  
 Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe  
 805 810 815

Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser  
 820 825 830  
 Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp  
 835 840 845  
 His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser  
 850 855 860  
 10 Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met  
 865 870 875 880  
 Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn  
 885 890 895  
 Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr  
 900 905 910  
 20 Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn  
 915 920 925  
 Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala  
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 Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His  
 945 950 955 960  
 Cys Thr Phe  
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 Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr  
 35 40 45  
 Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn  
 50 55 60  
 Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly  
 65 70 75 80  
 50 Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu  
 85 90 95  
 Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr  
 100 105 110



Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro  
 115 120 125  
 Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met  
 130 135 140  
 Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp  
 145 150 155 160  
 10 Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser  
 165 170 175  
 Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp  
 180 185 190  
 Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr  
 195 200 205  
 20 Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His  
 210 215 220  
 Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser  
 225 230 235 240  
 Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr  
 245 250 255  
 30 Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser  
 260 265 270  
 Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr  
 275 280 285  
 Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu  
 290 295 300  
 Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser  
 305 310 315 320  
 40 Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu  
 325 330 335  
 Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser  
 340 345 350  
 Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala  
 355 360 365  
 50 Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly  
 370 375 380  
 Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn  
 385 390 395 400  
 Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser  
 405 410 415

Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp  
                     420                    425                    430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu  
                     435                    440                    445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg  
                     450                    455                    460

10 Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu  
       465                    470                    475                    480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr  
                     485                    490                    495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser  
                     500                    505                    510

Thr Pro

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       <213> Chlamydia pneumoniae

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30 Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe  
                     20                    25                    30

Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe  
                     35                    40                    45

Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu  
                     50                    55                    60

40 Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile  
       65                    70                    75                    80

Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu  
                     85                    90                    95

Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr  
                     100                    105                    110

Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln  
                     115                    120                    125

50 Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro  
       130                    135                    140

His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val  
       145                    150                    155                    160

Gly Gly His Arg Ile Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val  
 165 170 175  
 Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala  
 180 185 190  
 Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met  
 195 200 205  
 10 Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp  
 210 215 220  
 Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile  
 225 230 235 240  
 Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr  
 245 250 255  
 20 Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala  
 260 265 270  
 Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val  
 275 280 285  
 Leu  
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 30 <212> PRT  
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 Leu Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu  
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 40 Ser Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr  
 35 40 45  
 Ile Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala  
 50 55 60  
 Trp Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly  
 65 70 75 80  
 50 Ile Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu  
 85 90 95  
 Leu Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu  
 100 105 110  
 Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly  
 115 120 125

Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala  
130 135 140

Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys  
145 150 155 160

Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser  
165 170 175

10 His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr  
180 185 190

Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe  
195 200 205

Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe  
210 215 220

20 Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu  
225 230 235 240

Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu  
245 250 255

Glu Gln Cys Met Lys Val Leu Val Lys  
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30 <210> 26  
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Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile  
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40 Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala  
35 40 45

Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val  
50 55 60

Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile  
65 70 75 80

50 Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
85 90 95